



SEQUENCE LISTING

10> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE
DOMAINS AND DNAS ENCODING THESE PROTEINS

<130> GIN-6706CPUS

<140> 09/445,258

<141> 1999-12-01

<150> PCT/US98/02445

<151> 1998-06-03

<150> JP 9-144948

<151> 1997-06-03

<160> 67

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 382

<212> PRT

<213> Homo sapiens

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Gly	Ala	Met	Ser	Pro	Pro	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu	20	25	30	
Ser	Arg	Gly	Cys	Asn	Asp	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala	35	40	45	
Leu	Arg	Asp	Ile	Asn	Lys	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu	50	55	60	
Asn	Arg	Val	Asn	Asp	Ala	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	65	70	75	80
Leu	Phe	Tyr	Leu	Thr	Leu	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	85	90	95	
Arg	Lys	Lys	Ala	Trp	Gln	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	100	105	110	
Val	Tyr	Gly	Gln	Cys	Lys	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	115	120	125	
Val	Leu	Tyr	Leu	Ala	Ala	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	130	135	140	
Lys	Lys	Ile	Tyr	Met	Thr	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	145	150	155	160
Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	165	170	175	
Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	180	185	190	
Thr	Arg	Ala	Ser	Ser	Gln	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	195	200	205	
Tyr	Leu	Ile	Lys	Glu	Ser	Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	210	215	220	
Ser	Leu	Gln	Ser	Ser	Asp	Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	225	230	235	240

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TECH CENTER 1600/2900

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TECH CENTER 1600/2900

Leu	Thr	Arg	Thr	His	Trp	Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe
				245					250					255	
Phe	Glu	Ser	Gln	Ala	Pro	Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn
			260					265					270		
Gln	Lys	Pro	Thr	Asn	Leu	Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn
		275					280					285			
Thr	Pro	Pro	Thr	Asp	Ser	Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val
	290					295					300				
Gln	Tyr	Leu	Pro	Asp	Leu	Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro
305					310					315					320
Gln	Glu	Ala	Phe	Pro	Val	His	Leu	Asp	Leu	Thr	Thr	Asn	Pro	Gln	Gly
				325					330					335	
Glu	Thr	Leu	Asp	Ile	Ser	Phe	Leu	Phe	Leu	Glu	Pro	Met	Glu	Glu	Lys
			340					345					350		
Leu	Val	Val	Leu	Pro	Phe	Pro	Lys	Glu	Lys	Ala	Arg	Thr	Ala	Glu	Cys
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Pro	Gly	Pro	Ala	Gln	Asn	Ala	Ser	Pro	Leu	Val	Leu	Pro	Pro		
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 <213> Homo sapiens

<400> 2

Met	Trp	Leu	Tyr	Leu	Ala	Ala	Phe	Val	Gly	Leu	Tyr	Tyr	Leu	Leu	His
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Trp	Tyr	Arg	Glu	Arg	Gln	Val	Val	Ser	His	Leu	Gln	Asp	Lys	Tyr	Val
		20						25					30		
Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Leu	Ala	Arg	Gln
		35					40					45			
Leu	Asp	Ala	Arg	Gly	Leu	Arg	Val	Leu	Ala	Ala	Cys	Leu	Thr	Glu	Lys
	50					55					60				
Gly	Ala	Glu	Gln	Leu	Arg	Gly	Gln	Thr	Ser	Asp	Arg	Leu	Glu	Thr	Val
65					70					75					80
Thr	Leu	Asp	Val	Thr	Lys	Met	Glu	Ser	Ile	Ala	Ala	Ala	Thr	Gln	Trp
				85				90						95	
Val	Lys	Glu	His	Val	Gly	Asp	Arg	Gly	Leu	Trp	Gly	Leu	Val	Asn	Asn
			100					105					110		
Ala	Gly	Ile	Leu	Thr	Pro	Ile	Thr	Leu	Cys	Glu	Trp	Leu	Asn	Thr	Glu
		115					120					125			
Asp	Ser	Met	Asn	Met	Leu	Lys	Val	Asn	Leu	Ile	Gly	Val	Ile	Gln	Val
	130					135					140				
Thr	Leu	Ser	Met	Leu	Pro	Leu	Val	Arg	Arg	Ala	Arg	Gly	Arg	Ile	Val
145					150					155					160
Asn	Val	Ser	Ser	Ile	Leu	Gly	Arg	Val	Ala	Phe	Phe	Val	Gly	Gly	Tyr
				165				170						175	
Cys	Val	Ser	Lys	Tyr	Gly	Val	Glu	Ala	Phe	Ser	Asp	Ile	Leu	Arg	Arg
		180						185					190		
Glu	Ile	Gln	His	Phe	Gly	Val	Lys	Ile	Ser	Ile	Val	Glu	Pro	Gly	Tyr
		195					200					205			
Phe	Arg	Thr	Gly	Met	Thr	Asn	Met	Thr	Gln	Ser	Leu	Glu	Arg	Met	Lys
	210					215					220				
Gln	Ser	Trp	Lys	Glu	Ala	Pro	Lys	His	Ile	Lys	Glu	Thr	Tyr	Gly	Gln
225					230					235					240
Gln	Tyr	Phe	Asp	Ala	Leu	Tyr	Asn	Ile	Met	Lys	Glu	Gly	Leu	Leu	Asn
				245					250					255	
Cys	Ser	Thr	Asn	Leu	Asn	Leu	Val	Thr	Asp	Cys	Met	Glu	His	Ala	Leu
			260					265					270		
Thr	Ser	Val	His	Pro	Arg	Thr	Arg	Tyr	Ser	Ala	Gly	Trp	Asp	Ala	Lys

	275		280		285
Phe	Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr				
	290		295		300
Ile	Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val				
305		310		315	

<210> 3
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 <213> Homo sapiens

<400> 3

Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Val	Gln	Gln	Leu	Gly	Leu	Leu	Gly
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Cys	Leu	Gly	His	Gly	Ala	Leu	Val	Leu	Gln	Leu	Leu	Ser	Phe	Met	Leu
			20					25					30		
Leu	Ala	Gly	Val	Leu	Val	Ala	Ile	Leu	Val	Gln	Val	Ser	Lys	Val	Pro
			35				40						45		
Ser	Ser	Leu	Ser	Gln	Glu	Gln	Ser	Glu	Gln	Asp	Ala	Ile	Tyr	Gln	Asn
	50				55					60					
Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys
65				70					75						80
Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly
			85						90					95	
Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr
			100					105					110		
Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln
		115				120						125			
Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu
	130				135						140				
Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu
145				150					155						160
Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile
			165					170						175	
Tyr	Gln	Glu	Leu	Thr	Glu	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu
			180				185						190		
Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala
	195					200						205			
Ala	Val	Gly	Glu	Leu	Pro	Asp	Gln	Ser	Lys	Gln	Gln	Gln	Ile	Tyr	Gln
	210				215							220			
Glu	Leu	Thr	Asp	Leu	Lys	Thr	Ala	Phe	Glu	Arg	Leu	Cys	Arg	His	Cys
225				230					235						240
Pro	Lys	Asp	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn
			245					250					255		
Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Val	Thr	Ala	Cys	Gln	Glu	Val	Arg
		260					265						270		
Ala	Gln	Leu	Val	Val	Ile	Lys	Thr	Ala	Glu	Glu	Gln	Leu	Pro	Ala	Val
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Leu	Glu	Gln	Trp	Arg	Thr	Gln	Gln								
	290					295									

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 <213> Homo sapiens

<400> 4

Met	Cys	Thr	Gly	Lys	Cys	Ala	Arg	Cys	Val	Gly	Leu	Ser	Leu	Ile	Thr
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Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn
20 25 30
Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp
35 40 45
Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly
50 55 60
Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys
65 70 75 80
Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe
85 90 95
Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu
100 105 110
Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe
115 120 125
Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg
130 135 140
Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser
145 150 155 160
Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln
165 170 175
Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys
180 185 190
Gln Asp Thr Pro His
195

<210> 5
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<213> Homo sapiens

<400> 5
Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
1 5 10 15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
20 25 30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
35 40 45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
50 55 60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
65 70 75 80
Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
85 90 95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
100 105 110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
115 120 125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
130 135 140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
145 150 155 160
Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
165 170 175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
180 185 190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
195 200 205
Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
210 215 220

<210> 6
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 <213> Homo sapiens

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 Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg
 1 5 10 15
 Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly
 20 25 30
 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr
 35 40 45
 Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val
 50 55 60
 Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr
 65 70 75 80
 Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala
 85 90 95
 Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr
 100 105 110
 Gly Leu Ala Met Asp Met Gln Leu Met Ile Pro Leu Ile Met Ser
 115 120 125
 Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe
 130 135 140
 Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu
 145 150 155 160
 Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly
 165 170 175
 Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met
 180 185 190
 Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg
 195 200 205
 Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro
 210 215 220
 Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
 225 230 235 240
 Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
 245 250

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<400> 7
 Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser
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 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro
 20 25 30
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val
 35 40 45
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Leu Thr Tyr Gly Leu
 50 55 60
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg
 65 70 75 80
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly
 85 90 95
 Leu Ala Val Thr Ala Met Lys Ser Arg Pro
 100 105

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 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
 1 5 10 15
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
 20 25 30
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
 35 40 45
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
 50 55 60
 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
 65 70 75

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<400> 9
 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
 1 5 10 15
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
 20 25 30
 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala
 35 40 45
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
 50 55 60
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala
 65 70 75 80
 Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
 85 90 95
 Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His
 100 105 110
 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys
 115 120 125
 Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu
 130 135 140
 Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu
 145 150 155 160
 Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys
 165 170 175
 Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
 180 185 190
 Lys Glu Ala Phe Val Val Glu Glu Gly Val Gly Glu Thr Met Thr
 195 200 205
 Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
 210 215 220
 Gln Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu
 225 230 235 240
 Arg Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly
 245 250 255
 Thr Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr
 260 265 270
 Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg

	275		280		285										
Val	Ser	Ile	Ala	Glu	Leu	Ala	Gln	Ala	Ser	Asn	Ser	Leu	Ile	Ala	Trp
	290					295					300				
Gly	Arg	Glu	Ser	Pro	Ala	Gln	Ala	Pro	Ala						
305					310										

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 <213> Homo sapiens

<400> 10

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Glu	Ser	Gly	Gly	Leu	Leu	His	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu
		20						25				30			
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly
		35					40					45			
Asp	Gln	Pro	Ala	Ala	Ser	Gly	Asp	Ser	Asp	Asp	Asp	Glu	Pro	Pro	Pro
50						55					60				
Leu	Pro	Arg	Leu	Lys	Arg	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg
65					70					75				80	
Phe	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys
			85						90					95	
Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro
			100					105					110		
Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe
		115					120					125			
Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp
130						135					140				
Leu	Thr	Ala	Ala	Gln	Gln	Glu	Thr	Leu	Ser	Asp	Trp	Glu	Ser	Gln	Phe
145					150					155					160
Thr	Phe	Lys	Tyr	His	His	Val	Gly	Lys	Leu	Leu	Lys	Glu	Gly	Glu	Glu
				165					170					175	
Pro	Thr	Val	Tyr	Ser	Asp	Glu	Glu	Glu	Pro	Lys	Asp	Glu	Ser	Ala	Arg
			180					185						190	
Lys	Asn	Asp													
		195													

<210> 11
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 <213> Homo sapiens

<400> 11

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu	Val
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Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	Gly	Ile
		20						25				30			
Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	Pro	Asp	Ile
		35					40					45			
Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	Leu	His	Glu	Arg
50						55					60				
Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	Arg	Leu	Val	Val	Ser
65					70					75				80	
Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	Ile	Asn	Pro	Asn	Lys	Thr
				85					90					95	
Leu	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	Ser	Leu	Leu	Arg	Tyr	Gln	Ser
			100					105					110		

Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	Leu	Tyr	Glu		
	115					120					125						
Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys		
	130					135					140						
Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln		
	145				150				155						160		
His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val		
			165				170							175			
Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile		
		180					185						190				
Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly		
	195					200						205					
Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr		
	210					215					220						
Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys		
	225				230					235					240		
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	Leu		
			245					250						255			
Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	Met	Ile		
		260					265						270				
Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	Thr	Trp	Ala		
	275					280						285					
Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	Leu	Tyr	Glu		
	290					295				300							
Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	Glu	Lys	Ile		
	305				310					315					320		
Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	Val	Arg	Thr		
			325						330					335			
Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	Glu	Gly	Lys		
		340					345						350				
Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu		
	355					360						365					
Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe		
	370				375						380						
Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser		
	385				390					395					400		
Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr		
			405					410						415			
Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu		
		420					425						430				
Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr		
		435				440						445					
Ser	Ser	Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
	450					455					460						

<210> 12
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 <213> Homo sapiens

<400> 12

Met	Gly	Ala	Ala	Val	Phe	Phe	Gly	Cys	Thr	Phe	Val	Ala	Phe	Gly	Pro		
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Ala	Phe	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	Arg	Val		
		20					25						30				
Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	Leu	Leu	Leu		
		35				40						45					
Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp		
	50					55					60						
Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val		

65					70					75					80
Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys
				85					90					95	
Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile
			100						105					110	
Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile
		115					120					125			
Ser	Gly	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro
	130					135					140				
Gly	Val	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser
145				150					155						160
Ala	Phe	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val
				165					170					175	
Val	Phe	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu
			180					185					190		
Val	Val	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro
	195					200						205			
Trp	Tyr	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met
	210				215						220				
Gly	Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln
225					230				235						240
Arg	Ser	Leu	Leu	Cys	Lys	Asp									
				245											

<210> 13
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 <212> PRT
 <213> Homo sapiens

<400> 13

Met	Asn	Phe	Tyr	Leu	Leu	Leu	Ala	Ser	Ser	Ile	Leu	Cys	Ala	Leu	Ile
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Val	Phe	Trp	Lys	Tyr	Arg	Arg	Phe	Gln	Arg	Asn	Thr	Gly	Glu	Met	Ser
			20					25					30		
Ser	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Val	Arg	Pro	Ser	Ser	Ser	Gly	Leu
		35				40						45			
Ile	Asn	Ser	Asn	Thr	Asp	Asn	Asn	Leu	Ala	Val	Tyr	Asp	Leu	Ser	Arg
	50				55						60				
Asp	Ile	Leu	Asn	Asn	Phe	Pro	His	Ser	Ile	Ala	Arg	Gln	Lys	Arg	Ile
65				70						75					80
Leu	Val	Asn	Leu	Ser	Met	Val	Glu	Asn	Lys	Leu	Val	Glu	Leu	Glu	His
			85						90					95	
Thr	Leu	Leu	Ser	Lys	Gly	Phe	Arg	Gly	Pro	Ser	Pro	His	Arg	Lys	Ser
			100					105					110		

Thr

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 <212> PRT
 <213> Homo sapiens

<400> 14

Met	Gly	Arg	Trp	Ala	Leu	Asp	Val	Ala	Phe	Leu	Trp	Lys	Ala	Val	Leu
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Thr	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Tyr	Cys	Phe	Ser	Ile	Gly	Ile	Thr
		20					25						30		
Phe	Tyr	Asn	Lys	Trp	Leu	Thr	Lys	Ser	Phe	His	Phe	Pro	Leu	Phe	Met
		35					40					45			

Thr	Met	Leu	His	Leu	Ala	Val	Ile	Phe	Leu	Phe	Ser	Ala	Leu	Ser	Arg	
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Ala	Leu	Val	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	
65					70					75					80	
Ala	Asp	Tyr	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	
				85					90					95		
Asp	Val	Gly	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	
			100					105					110			
Tyr	Thr	Met	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	
	115						120					125				
Leu	Ile	Phe	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	
	130					135					140					
Leu	Leu	Ile	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	
145					150					155					160	
Phe	Asn	Val	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	
			165						170					175		
Gly	Ile	Arg	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	
	180						185						190			
Gly	Leu	Gln	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	
	195						200					205				
Phe	Leu	Gly	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	
	210					215					220					
Ser	Thr	Ser	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	
225					230					235					240	
Arg	Val	Leu	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	
			245						250					255		
Gly	Phe	Ser	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	
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Ser	Ile	Ala	Gly	Ile	Phe	Lys	Glu	Val	Cys	Thr	Leu	Leu	Leu	Ala	Ala	
	275						280					285				
His	Leu	Leu	Gly	Asp	Gln	Ile	Ser	Leu	Leu	Asn	Trp	Leu	Gly	Phe	Ala	
	290					295					300					
Leu	Cys	Leu	Ser	Gly	Ile	Ser	Leu	His	Val	Ala	Leu	Lys	Ala	Leu	His	
				310						315					320	
Ser	Arg	Gly	Asp	Gly	Gly	Pro	Lys	Ala	Leu	Lys	Gly	Leu	Gly	Ser	Ser	
			325						330					335		
Pro	Asp	Leu	Glu	Leu	Leu	Leu	Arg	Ser	Ser	Gln	Arg	Glu	Glu	Gly	Asp	
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Asn	Glu	Glu	Glu	Glu	Tyr	Phe	Val	Ala	Gln	Gly	Gln	Gln				
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 <212> PRT
 <213> Homo sapiens

<400> 15

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			20					25					30			
Trp	Ile	Thr	Ser	Thr	Ile	Ala	Val	Arg	Asp	Ser	Ala	Ser	Asn	Gly	Ser	
		35				40						45				
Ile	Phe	Ile	Thr	Tyr	Gly	Leu	Phe	Arg	Gly	Glu	Ser	Ser	Glu	Glu	Leu	
	50				55					60						
Ser	His	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Lys	Phe	Ala	Val	Leu	Glu	Ile	
65					70					75				80		
Leu	Asn	Asn	Ser	Ser	Gln	Lys	Thr	Leu	His	Ser	Val	Thr	Ile	Leu	Phe	
			85					90					95			
Leu	Val	Leu	Ser	Leu	Ile	Thr	Ser	Leu	Leu	Ser	Ser	Gly	Phe	Thr	Phe	

			100					105					110			
Tyr	Asn	Ser	Ile	Ser	Asn	Pro	Tyr	Gln	Thr	Phe	Leu	Gly	Pro	Thr	Gly	
		115					120					125				
Val	Tyr	Thr	Trp	Asn	Gly	Leu	Gly	Ala	Ser	Phe	Val	Phe	Val	Thr	Met	
		130					135					140				
Ile	Leu	Phe	Val	Ala	Asn	Thr	Gln	Ser	Asn	Gln	Leu	Ser	Glu	Glu	Leu	
145					150					155					160	
Phe	Gln	Met	Leu	Tyr	Pro	Ala	Thr	Thr	Ser	Lys	Gly	Thr	Thr	His	Ser	
				165					170					175		
Tyr	Gly	Tyr	Ser	Phe	Trp	Leu	Ile	Leu	Leu	Val	Ile	Leu	Leu	Asn	Ile	
			180					185					190			
Val	Thr	Val	Thr	Ile	Ile	Ile	Phe	Tyr	Gln	Lys	Ala	Arg	Tyr	Gln	Arg	
		195					200					205				
Lys	Gln	Glu	Gln	Arg	Lys	Pro	Met	Glu	Tyr	Ala	Pro	Arg	Asp	Gly	Ile	
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Leu	Phe															
225																

<210> 16
 <211> 129
 <212> PRT
 <213> Homo sapiens

Met	Ala	Arg	Gly	Ser	Leu	Arg	Arg	Leu	Leu	Arg	Leu	Leu	Val	Leu	Gly	
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Leu	Trp	Leu	Ala	Leu	Leu	Arg	Ser	Val	Ala	Gly	Glu	Gln	Ala	Pro	Gly	
		20						25					30			
Thr	Ala	Pro	Cys	Ser	Arg	Gly	Ser	Trp	Ser	Ala	Asp	Leu	Asp	Lys		
		35					40				45					
Cys	Met	Asp	Cys	Ala	Ser	Cys	Arg	Ala	Arg	Pro	His	Ser	Asp	Phe	Cys	
	50					55					60					
Leu	Gly	Cys	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Phe	Arg	Leu	Leu	Trp	Pro	
65				70						75					80	
Ile	Leu	Gly	Gly	Ala	Leu	Ser	Leu	Thr	Phe	Val	Leu	Gly	Leu	Leu	Ser	
			85						90					95		
Gly	Phe	Leu	Val	Trp	Arg	Arg	Cys	Arg	Arg	Arg	Glu	Lys	Phe	Thr	Thr	
		100						105					110			
Pro	Ile	Glu	Glu	Thr	Gly	Gly	Glu	Gly	Cys	Pro	Ala	Val	Ala	Leu	Ile	
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Gln																

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 <212> PRT
 <213> Homo sapiens

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		20						25					30			
Ala	Leu	Glu	Glu	Phe	His	Lys	His	Pro	Pro	Val	Gln	Trp	Ala	Phe	Gln	
		35					40					45				
Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	Ala	Gly	Ile	
	50					55					60					
Phe	Val	Arg	Leu	Glu	Phe	Lys	Leu	Gln	Gln	Thr	Ser	Cys	Arg	Lys	Arg	
65					70					75					80	

Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg
85 90 95
Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly
100 105 110
Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu
115 120 125
Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp
130 135 140
Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu
145 150 155 160
Pro Arg Ser

<210> 18
<211> 193
<212> PRT
<213> Homo sapiens

<400> 18
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20 25 30
Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45
Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60
Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65 70 75 80
Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
85 90 95
Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
100 105 110
Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile
115 120 125
Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Arg Ala
130 135 140
Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160
Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175
Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190
Ala

<210> 19
<211> 1146
<212> DNA
<213> Homo sapiens

<400> 19
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ccaccccgagc tggccctcaa cccctcggct ctgctctccc ggggctgcaa tgactccgat 120
gtgctggcagc ttgcaggctt tgccctgcgg gatattaaca aagacagaaa ggatggctat 180
gtgctgagac tcaaccgagt gaacgacgcc caggaataca gacggggtgg cctgggatct 240
ctgttctatc ttacactgga tgtgctagag actgactgcc atgtgctcag aaagaaggca 300
tggcaagact gtggaatgag gatatttttt gaatcagttt atggtcaatg caaagcaata 360
ttttatatga acaaccaag tagagttctc tatttagctg cttataactg tactcttcgc 420

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ccagtttcaa aaaaaaagat ttacatgacg tgccttgact gcccaagctc catacccact 480
gactcttcca atcaccaagt gctggagggt gccaccgagt ctcttgcgaa atacaacaat 540
gagaacacat ccaagcagta ttctctcttc aaagtcacca gggcttctag ccagtgggtg 600
gtcggccctt cttactttgt ggaatactta attaaagaat caccatgtac taaatcccag 660
gccagcagct gttcacttca gtctctcgac tctgtgcctg ttggtctttg caaaggttct 720
ctgactcgaa cacactggga aaagtttgto tctgtgactt gtgacttctt tgaatcacag 780
gctccagcca ctggaagtga aaactctgct gttaaccaga aacctacaaa ccttcccag 840
gtggaagaat cccagcagaa aaacaccccc ccaacagact cccctccaa agctgggcca 900
agaggatctg tccaatatct tctgacttg gatgataaaa attcccagga aaagggcct 960
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atttcttcc tcttctgga gcctatggag gagaagctgg ttgtcctgcc tttcccaaaa 1080
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<210> 20

<211> 951

<212> DNA

<213> Homo sapiens

<400> 20

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tttgggaacc tgctggccag acagctggat gcacgaggct tgagagtgtt ggctgcgtgt 180
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gtgggggaca gaggactctg gggactggtg aacaatgcag gcattcttac accaattacc 360
ttatgtgagt ggctgaacac tgaggactct atgaatatgc tcaaagttaa cctcatttgt 420
gtgatccagg tgaccttgag catgcttctt ttggtgagga gagcacgggg aagaattgtc 480
aatgtctcca gcattctggg aagagttgct ttctttgtag gaggctactg tgtctccaag 540
tatggagtgg aagccttttc agatattctg aggcgtgaga ttcaacattt tggggtgaaa 600
atcagcatag ttgaacctgg ctacttcaga acgggaatga caaacatgac acagtcctta 660
gagcgaatga agcaaaagtg gaaagaagcc cccaagcata ttaaggagac ctatggacag 720
cagtatcttg atgcccttta caatatcatg aagggaaggc tgttgaattg tagcacaac 780
ctgaacctgg tcaactgactg catggaacat gctctgacat cgggtgcatc gcgaactcga 840
tattcagctg gctgggatgc taaatttttc ttcacccctc tatcttattt acctacatca 900
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<210> 21

<211> 888

<212> DNA

<213> Homo sapiens

<400> 21

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cttgtccaag tgtccaaggt ccccagctcc ctaagtcagg aacaatccga gcaagacgca 180
atctaccaga acctgaccga gcttaaagct gcagtgggtg agctctcaga gaaatccaag 240
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gtgggtgagt tgccagagaa atccaagctg caggagatct accaggagct gacccggctg 480
aaggctgcag tgggtgagtt gccagagaaa tccaagctgc aggagatcta ccaggagctg 540
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caggagctga cccagctgaa ggctgcagtg ggtgagttgc cagaccagtc caagcagcag 660
caaactctatc aagaactgac cgatttgaag actgcatttg aacgcctgtg ccgccaactgt 720
cccaaggact ggacattctt ccaaggaaac tgttacttca tgtctaactc ccagcggaac 780
tggcacgact ccgtcaccgc ctgccaggaa gtgagggccc agctcgtcgt aatcaaaact 840
gctgaggagc agcttccagc ggtactggaa cagtggagaa cccaacaa 888

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<210> 22

<211> 591

<212> DNA
<213> Homo sapiens

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aaccatctca gcttgcaagt ctggctcatg ggcggcttca ttggcggggg cctaattgta 180
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ctatgggatc ggtgcgaggc gccccctcgc gtggtccctt ggaatgtgac gctcttctcg 480
ctgctggtgg ccgctcctg cctggagata gtactgtgtg ggatccagct ggtgaacgcg 540
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<210> 23
<211> 663
<212> DNA
<213> Homo sapiens

<400> 23
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aacgtccagt tctgcccctt tctcaccacg gaagtcaaca acctgggctg gctgagttat 180
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tacctctcac cactggctga cttggctaag gtgattcaaa ctaaataaac ccaatgtctc 480
tctacccac tcaccattgc tacccttctc acctctgctt cctggtgctt ctatgggttt 540
cgactcagag atccctatat catggtgtcc aactttccag gaatcgtcac cagctttatc 600
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acc 663

<210> 24
<211> 753
<212> DNA
<213> Homo sapiens

<400> 24
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ctctggcccc aagccttctt ttatcgcttt cagatttgga ggccaatcac tgccaccttt 180
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cagtattcta cgcgacttga aacaggagct tttgatggga ggccagcaga ctattttattc 300
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ctgatgattc ctctgatcat gtcagtactt tatgtctggg ccagctgaa cagagacatg 420
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ggattcaact atatcatcgg aggtcggta atcaatgagc ttattggaaa tctggttgga 540
catctttatt ttttctaat gttcagatac ccaatggact tgggaggaag aaattttcta 600
tocacacctc agtttttgta ccgctggctg ccagtagga gaggaggagt atcaggattt 660
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aactggggcc agggctttcg acttgagac cag 753

<210> 25
<211> 318
<212> DNA
<213> Homo sapiens

<400> 25
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cgcaagacccc gcgagaacccc ggtgggtaccc atagggtgcc tggccacggc ggccgccttc 180
acctacgggcc tctactcctt ccaccggggc aacagccagc gctctcagct catgatgcgc 240
acccgcatcg ccgcccaggg tttcacggtc gcagccatct tgctgggtct ggctgtcact 300
gctatgaagt ctgcaccc                                     318

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<210> 26
 <211> 234
 <212> DNA
 <213> Homo sapiens

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<400> 26
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gagtcagct tcttggaatt gcttgaaaag ctctgcctcc tcctccatct cccttcaggg 180
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<210> 27
 <211> 942
 <212> DNA
 <213> Homo sapiens

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<400> 27
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ctggcaggag caggccgggt ggcccagcct gggcccctgg agcctgagga gccgagagct 180
ggaggcaggc ctcggcgccg gagggacctg ggcagccgcc tacaggccca gcgtcgagcc 240
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gaggaggaag gtgtcgagaa gccagcggaa actcacctgt cggggaaaat tggagctaag 360
aaactgcgga agctggagga gaaacaagcg cgaaaggccc agcgtgaggc agaggaggct 420
gaacgtgagg agcggaaacg actcgagtcc cagcgcgaag ctgagtggaa gaaggaggag 480
gagcggcttc gcctggagga ggagcagaag gaggaggagg agaggaaggc ccgcgaggag 540
caggcccagc gggagcatga ggagtacctg aaactgaagg aggcctttgt ggtggaggag 600
gaaggcgtag gagagaccat gactgaggaa cagtcaccga gcttcctgac agagttcatc 660
aactacatca agcagtccaa ggttgtgtctc ttggaagacc tggcttccca ggtgggccta 720
cgcactcagg acaccataaa tcgcatccag gacctgctgg ctgaggggac tataacaggt 780
gtgattgacg accggggcaa gttcatctac ataaccccag aggaactggc cgccgtggcc 840
aacttcatcc gacagcgggg ccgggtgtcc atcgccgagc ttgcccaagc cagcaactcc 900
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<210> 28
 <211> 585
 <212> DNA
 <213> Homo sapiens

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<400> 28
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ctgctctaca agatcgtgcg cggggaccag ccggcgccca gcggcgacag cgacgacgac 180
gagccgcccc ctctgccccg cctcaagcgg cgcgacttca ccccgcgca gctgcggcgc 240
ttcgacggcg tccaggacct gcgcatactc atggccatca acggcaaggt gttcgatgtg 300
accaaaggcc gcaaattcta cgggcccag gggccgtatg ggtctttgc tggaaagat 360
gcatccaggg gccttgccac attttgctg gataaggaa cactgaagga tgagtacgat 420
gacctttctg acctcactgc tgcccagcag gagactctga gtgactggga gtctcagttc 480
actttcaagt atcatcacgt gggcaaactg ctgaaggagg gggaggagcc cactgtgtac 540
tcagatgagg aagaacccaa agatgagagt gcccgaaaa atgat 585

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<210> 29
 <211> 1386
 <212> DNA
 <213> Homo sapiens

<400> 29

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aaagatggta	atcttccaga	tattgtgaat	agtggaaagt	tgcattgagt	cctgggtaat	180
ttgcatgaga	gatatgggcc	tgtggtctcc	ttctggtttg	gcaggcgcc	cgtgggttagt	240
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gaaaccatgc	tgaagtcatt	attaaggtat	caatctggtg	gtggcagtgt	gagtgaaaac	360
cacatgagga	aaaaattgta	tgaaaatggt	gtgactgatt	ctctgaagag	taactttgcc	420
ctcctcctaa	agctttcaga	agaattatta	gataaatggc	tctcctaccc	agagaccag	480
cacgtgcccc	tcagccagca	tatgcttggg	tttgctatga	agtctgttac	acagatggta	540
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gtttggtctg	agattggaag	aggctttcta	gatgggtcac	ttgataaaaa	catgactcgg	660
aaaaaacaat	atgaagatgc	cctcatgcaa	ctggagctctg	ttttaaggaa	catcataaaa	720
gaacgaaaag	gaaggaactt	cagtcaacat	atcttcattg	actccttagt	acaagggaac	780
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aaattatatg	aagagataaa	ccaagttttt	ggaaatggct	ctgttactcc	agagaaaatt	960
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gagaccctcg	tcctttatgc	ccttggtgtg	gtacttcagg	atcctaatac	ttggccatct	1140
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gtactttcta	gtgtattggt	gaagagactg	cacctacttt	ctgtggaggg	acagggttatt	1320
gaaacaaagt	atgaactggt	aacatcatca	agggaagaag	cttggatcac	tgtctcaaag	1380
agatat						1386

<210> 30

<211> 741

<212> DNA

<213> Homo sapiens

<400> 30

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ttctggctgg	tctccctgct	cctggcctct	gtgggtctgg	tcattcttgg	ccatgtgacc	180
gaccggctag	atgcccggt	ccagtacggc	ctcctgattt	ttgggtgctg	tgtctctgtc	240
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ttagcatcgc	tgagtgagga	cggaaagatca	cccatctcca	tccgccagat	ggcctatgtt	360
tctggtctct	ccttcggtat	catcagtggg	gtcttctctg	ttatcaatat	tttggtgat	420
gcacttgggc	caggtgtggg	tgggatccat	ggagactcac	cctattactt	cctgacttca	480
gcctttctga	cagcagccat	tatcctgctc	catacctttt	ggggagttgt	gttctttgat	540
gcctgtgaga	ggagacggta	ctgggctttg	ggcctgggtg	ttgggagtca	cctactgaca	600
tcgggactga	cattcctgaa	cccctgggtat	gaggccagcc	tgctgcccat	ctatgcagtc	660
actgtttcca	tggggctctg	ggccttcac	acagctggag	ggtccctccg	aagtattcag	720
cgcagcctct	tgtgtaagga	c				741

<210> 31

<211> 339

<212> DNA

<213> Homo sapiens

<400> 31

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tatcgccgct	ttcagagaaa	cactggcgaa	atgtcatcaa	attcaactgc	tcttgacta	120
gtgagaccct	cttcttctgg	gttaattaac	agcaatacag	acaacaatct	tgcagtctac	180
gacctctctc	gggatatttt	aaataatttc	ccacactcaa	tagccaggca	gaagcgaata	240
ttggtaaacc	tcagtatggt	ggaaaacaag	ctggttgaac	tggaaacatac	tctacttagc	300
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<210> 32

<211> 1095
 <212> DNA
 <213> Homo sapiens

<400> 32
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 agcttccatt tccccctctt catgacgatg ctgcacctgg ccgtgatctt cctcttctcc 180
 gccctgtcca gggcgctggt tcagtgtctc agccacaggg ccctgtgtgt gctgagctgg 240
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 gtcttggtgg tcctcctcat cgccgggggt ctcttcatgt tcacctaca gtccacacag 480
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 ggtctccatt tgtccacatc tgagaaaatc ttccgtttcc aggacacagg gctgctcctg 720
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 gccagggggc agcag 1095

<210> 33
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 33
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 agagactctg cttcaaatgg gagcattttc atcacttacg gactttttcg tggggagagt 180
 agtgaagaat tgagtcacgg acttgacaga ccaaagaaaa agtttgcagt tttagagata 240
 ctgaataatt cttcccaaaa aactctgcat tcgggtgacta tcctgttctt ggtcctgagt 300
 ttgatcacgt cgctgctgag ctctgggttt accttctaca acagcatcag caaccttac 360
 cagacattcc tggggccgac ggggggtgtac acctggaacg ggctcgggtc atccttogtt 420
 tttgtgacca tgatactgtt tgtggcgaac acgcagtcca accaactctc cgaagagttg 480
 ttccaaatgc tttaccgggc aaccaccagt aaaggaacga cccacagtta cggatactcg 540
 ttctggctca tactgctcgt cattcttcta aatatagtca ctgtaaccat catcattttc 600
 taccagaagg ccagatacca gcggaagcag gagcagagaa agccaatgga atatgctcca 660
 agggacggaa ttttattc 678

<210> 34
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 34
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 ttgctgcgct ccgtggccgg ggagcaagcg ccaggcaccg cccctgctc ccgcggcagc 120
 tcctggagcg cggacctgga caagtgcagt gactgcgcgt cttgcagggc gcgaccgcac 180
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 tggagacgat gccgcaggag agagaagttc accaccccca tagaggagac cggcggagag 360
 ggctgcccgat ctgtggcgct gatccag 387

<210> 35
 <211> 489
 <212> DNA

<213> Homo sapiens

<400> 35

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ccgcccgtgc agtgggcctt ccaggagacc agtgtggaga gcgccgtgga cacgcccttc 180
ccagctggaa tatttgtgag gctggaattt aagctgcagc agacaagctg ccggaagagg 240
gactggaaga aacccgagtg caaagtcagg cccaatggga ggaaacggaa atgcctggcc 300
tgcataaac tgggctctga ggacaaagtt ctgggcccgt tggctcactg ccccatagag 360
acccaagttc tgcgggagcg tgaggagcac caggagaccc agtgcctcag ggtgcagcgg 420
gctggtgagg acccccacag cttctacttc cctggacagt tcgccttctc caaggccctg 480
ccccgcagc                                     489

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<210> 36

<211> 579

<212> DNA

<213> Homo sapiens

<400> 36

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cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
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gccaacctgt ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga tcggtgtgtc cttcttcttc tgcctcctcc ccaactacga agatgacctt 540
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<210> 37

<211> 1502

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)...(1185)

<400> 37

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                                         Met Gly Leu Leu Leu Pro
                                         1                               5

ctg gca ctc tgc atc cta gtc ctg tgc tgc gga gca atg tct cca ccc 102
Leu Ala Leu Cys Ile Leu Val Leu Cys Cys Gly Ala Met Ser Pro Pro
                        10                        15                        20

cag ctg gcc ctc aac ccc tcg gct ctg ctc tcc cgg ggc tgc aat gac 150
Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp
                        25                        30                        35

tcc gat gtg ctg gca gtt gca ggc ttt gcc ctg cgg gat att aac aaa 198
Ser Asp Val Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys
                        40                        45                        50

gac aga aag gat ggc tat gtg ctg aga ctc aac cga gtg aac gac gcc 246
Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala
                        55                        60                        65                        70

cag gaa tac aga cgg ggt ggc ctg gga tct ctg ttc tat ctt aca ctg 294

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Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	Leu	Phe	Tyr	Leu	Thr	Leu	
				75					80					85		
gat	gtg	cta	gag	act	gac	tgc	cat	gtg	ctc	aga	aag	aag	gca	tgg	caa	342
Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	Arg	Lys	Lys	Ala	Trp	Gln	
			90					95					100			
gac	tgt	gga	atg	agg	ata	ttt	ttt	gaa	tca	gtt	tat	ggg	caa	tgc	aaa	390
Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	Val	Tyr	Gly	Gln	Cys	Lys	
		105					110					115				
gca	ata	ttt	tat	atg	aac	aac	cca	agt	aga	gtt	ctc	tat	tta	gct	gct	438
Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	Val	Leu	Tyr	Leu	Ala	Ala	
	120					125					130					
tat	aac	tgt	act	ctt	cgc	cca	gtt	tca	aaa	aaa	aag	att	tac	atg	acg	486
Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	Lys	Lys	Ile	Tyr	Met	Thr	
135					140					145					150	
tgc	cct	gac	tgc	cca	agc	tcc	ata	ccc	act	gac	tct	tcc	aac	cac	caa	534
Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	Asp	Ser	Ser	Asn	His	Gln	
				155					160					165		
gtg	ctg	gag	gct	gcc	acc	gag	tct	ctt	gcg	aaa	tac	aac	aac	gag	aac	582
Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	Lys	Tyr	Asn	Asn	Glu	Asn	
			170					175					180			
aca	tcc	aag	cag	tat	tct	ctc	ttc	aaa	gtc	acc	agg	gct	tct	agc	cag	630
Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	Thr	Arg	Ala	Ser	Ser	Gln	
		185					190					195				
tgg	gtg	gtc	ggc	cct	tct	tac	ttt	gtg	gaa	tac	tta	att	aaa	gaa	tca	678
Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	Tyr	Leu	Ile	Lys	Glu	Ser	
	200					205					210					
cca	tgt	act	aaa	tcc	cag	gcc	agc	agc	tgt	tca	ctt	cag	tcc	tcc	gac	726
Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	Ser	Leu	Gln	Ser	Ser	Asp	
215					220				225						230	
tct	gtg	cct	gtt	ggg	ctt	tgc	aaa	ggg	tct	ctg	act	cga	aca	cac	tgg	774
Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	Leu	Thr	Arg	Thr	His	Trp	
				235					240					245		
gaa	aag	ttt	gtc	tct	gtg	act	tgt	gac	ttc	ttt	gaa	tca	cag	gct	cca	822
Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe	Phe	Glu	Ser	Gln	Ala	Pro	
			250					255					260			
gcc	act	gga	agt	gaa	aac	tct	gct	gtt	aac	cag	aaa	cct	aca	aac	ctt	870
Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn	Gln	Lys	Pro	Thr	Asn	Leu	
		265					270					275				
ccc	aag	gtg	gaa	gaa	tcc	cag	cag	aaa	aac	acc	ccc	cca	aca	gac	tcc	918
Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn	Thr	Pro	Pro	Thr	Asp	Ser	
	280					285					290					
ccc	tcc	aaa	gct	ggg	cca	aga	gga	tct	gtc	caa	tat	ctt	cct	gac	ttg	966
Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val	Gln	Tyr	Leu	Pro	Asp	Leu	
295					300				305						310	
gat	gat	aaa	aac	tcc	cag	gaa	aag	ggc	cct	cag	gag	gcc	ttt	cct	gtg	1014
Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro	Gln	Glu	Ala	Phe	Pro	Val	

315	320	325	
cat ctg gac cta acc acg aat ccc cag gga gaa acc ctg gat att tcc			1062
His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser			
330	335	340	
ttc ctc ttc ctg gag cct atg gag gag aag ctg gtt gtc ctg cct ttc			1110
Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe			
345	350	355	
ccc aaa gaa aaa gca cgc act gct gag tgc cca ggg cca gcc cag aat			1158
Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn			
360	365	370	
gcc agc cct ctt gtc ctt ccg cca tga gaatcacaca gagtcttctg			1205
Ala Ser Pro Leu Val Leu Pro Pro *			
375	380		
taggggtatg gtgcgccgca tgacatggga ggcgatgggg acgatggaca gagacagagc			1265
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actgccttgt accctgagct gcatcacctc ctaaactgag cagtctcata ccatggagag			1445
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		Met Trp	
		1	
ctc tac ctg gcg gcc ttc gtg ggc ctg tac tac ctt ctg cac tgg tac			164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr			
5	10	15	
cgg gag agg cag gtg gtg agc cac ctc caa gac aag tat gtc ttt atc			212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile			
20	25	30	
acg ggc tgt gac tcg ggc ttt ggg aac ctg ctg gcc aga cag ctg gat			260
Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp			
35	40	45	50
gca cga ggc ttg aga gtg ctg gct gcg tgt ctg acg gag aag ggg gcc			308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala			
55	60	65	
gag cag ctg agg ggc cag acg tct gac agg ctg gag acg gtg acc ctg			356
Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu			
70	75	80	
gat gtt acc aag atg gag agc atc gct gca gct act cag tgg gtg aag			404
Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys			

21

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ttgccttatt aaacagagta gatggaaaac aattt 1349

<210> 39
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25)...(915)

<400> 39
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Met Ser Asp Ser Lys Glu Pro Arg Val
1 5

cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg 99
Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
10 15 20 25

caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt 147
Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
30 35 40

gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag 195
Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
45 50 55

caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt 243
Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly
60 65 70

gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc 291
Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
75 80 85

cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag 339
Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
90 95 100 105

gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg 387
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
110 115 120

cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg 435
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
125 130 135

aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc 483
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
140 145 150

tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag 531
Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
155 160 165

aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct 579
Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Thr Glu Leu Lys Ala
170 175 180 185

gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag 627
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
190 195 200

gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc 675
Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
205 210 215

aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt 723
Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
220 225 230

gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga 771
Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly
235 240 245

aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc 819
Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val
250 255 260 265

acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct 867
Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala
270 275 280

gag gag cag ctt cca gcg gta ctg gaa cag tgg aga acc caa caa tag 915
Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln *
285 290 295

cggggaatgaa gactgtgcgg aatttagtgg cagtggctgg aacgacaatc gatgtgacgt 975
tgacaattac tggatctgca aaaagccgc agcctgcttc agagacgaat agttgtttcc 1035
ctgctagcct cagcctccat tgtggtatag cagaacttca cccacttgta agccagcgct 1095
tcttctctcc atccttggac cttcacaaat gccctgagac ggttctctgt tcgatttttc 1155
atccccatg aacctgggtc ttattctgtc cttctgatgc ctccaagttt cctgggtgta 1215
gagcttgtgt tcttggccca tccttgagc tttataagtg acctgagtgg gatgcattta 1275
gggggcgggc ttggtatgtt gtatgaatcc actctctgtt ccttttggag attagactat 1335
ttggattcat gtgtagctgc cctgtccct ggggctttat ctcatccatg caaactacca 1395
tctgtcaac ttccagctac accccgtgca cccttttgac tggggacttg ctgggtgaag 1455
gagctcatct tgcaggctgg aagcaccagg gaattaattc cccagtcaa ccaatggcat 1515
ccagagaggg catggaggct ccatacaacc tcttccaccc ccacatctt ctttgtccta 1575
tacatgtctt ccatttggct gtttctgagt tgtagccttt ataataaagt ggtaaatgtt 1635
gtaactgc 1643

<210> 40
<211> 729
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (38)...(631)

<400> 40
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Met Cys Thr Gly Lys Cys
1 5

gcc cgc tgt gtg ggg ctc tcc ctc att acc ctc tgc ctc gtc tgc att 103
Ala Arg Cys Val Gly Leu Ser Leu Ile Thr Leu Cys Leu Val Cys Ile
10 15 20

gtg gcc aac gcc ctc ctg ctg gta cct aat ggg gag acc tcc tgg acc 151

Val	Ala	Asn	Ala	Leu	Leu	Leu	Val	Pro	Asn	Gly	Glu	Thr	Ser	Trp	Thr		
		25					30					35					
aac	acc	aac	cat	ctc	agc	ttg	caa	gtc	tgg	ctc	atg	ggc	ggc	ttc	att	199	
Asn	Thr	Asn	His	Leu	Ser	Leu	Gln	Val	Trp	Leu	Met	Gly	Gly	Phe	Ile		
	40					45				50							
ggc	ggg	ggc	cta	atg	gta	ctg	tgt	ccg	ggg	att	gca	gcc	ggt	cgg	gca	247	
Gly	Gly	Gly	Leu	Met	Val	Leu	Cys	Pro	Gly	Ile	Ala	Ala	Val	Arg	Ala		
	55				60					65					70		
ggg	ggc	aag	ggc	tgc	tgt	ggt	gct	ggg	tgc	tgt	gga	aac	cgc	tgc	agg	295	
Gly	Gly	Lys	Gly	Cys	Cys	Gly	Ala	Gly	Cys	Cys	Gly	Asn	Arg	Cys	Arg		
			75						80					85			
atg	ctg	cgc	tgc	gtc	ttc	tcc	tgc	gcg	ttc	ggg	gtg	ctt	ggt	gcc	atc	343	
Met	Leu	Arg	Ser	Val	Phe	Ser	Ser	Ala	Phe	Gly	Val	Leu	Gly	Ala	Ile		
			90					95					100				
tac	tgc	ctc	tgc	gtg	tct	gga	gct	ggg	ctc	cga	aat	gga	ccc	aga	tgc	391	
Tyr	Cys	Leu	Ser	Val	Ser	Gly	Ala	Gly	Leu	Arg	Asn	Gly	Pro	Arg	Cys		
		105					110					115					
tta	atg	aac	ggc	gag	tgg	ggc	tac	cac	ttc	gaa	gac	acc	gcg	gga	gct	439	
Leu	Met	Asn	Gly	Glu	Trp	Gly	Tyr	His	Phe	Glu	Asp	Thr	Ala	Gly	Ala		
	120					125					130						
tac	ttg	ctc	aac	cgc	act	cta	tgg	gat	cgg	tgc	gag	gcg	ccc	cct	cgc	487	
Tyr	Leu	Leu	Asn	Arg	Thr	Leu	Trp	Asp	Arg	Cys	Glu	Ala	Pro	Pro	Arg		
	135				140					145					150		
gtg	gtc	ccc	tgg	aat	gtg	acg	ctc	ttc	tgc	ctg	ctg	gtg	gcc	gcc	tcc	535	
Val	Val	Pro	Trp	Asn	Val	Thr	Leu	Phe	Ser	Leu	Leu	Val	Ala	Ala	Ser		
				155					160					165			
tgc	ctg	gag	ata	gta	ctg	tgt	ggg	atc	cag	ctg	gtg	aac	gcg	acc	att	583	
Cys	Leu	Glu	Ile	Val	Leu	Cys	Gly	Ile	Gln	Leu	Val	Asn	Ala	Thr	Ile		
			170					175					180				
ggt	gtc	ttc	tgc	ggc	gat	tgc	agg	aaa	aaa	cag	gac	acc	cct	cac	tga	631	
Gly	Val	Phe	Cys	Gly	Asp	Cys	Arg	Lys	Lys	Gln	Asp	Thr	Pro	His	*		
		185					190					195					
ggctccactg	accgccgggt	tacacctget	ccttcctgga	cgctacctg	gctcgetcac	691											
tcccttgctc	gctagaataa	actgctttgc	gctctctt			729											

<210> 41
 <211> 1322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)...(749)

<400> 41
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 cgcggggatcc gactctagtc gta atg gag gcg ggc ggc ttt ctg gac tgc ctc 113
 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu
 1 5 10

att tac gga gca tgc gtg gtc ttc acc ctt ggc atg ttc tcc gcc ggc	161
Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
15 20 25	
ctc tcg gac ctc agg cac atg cga atg acc cgg agt gtg gac aac gtc	209
Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
30 35 40	
cag ttc ctg ccc ttt ctc acc acg gaa gtc aac aac ctg ggc tgg ctg	257
Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
45 50 55	
agt tat ggg gct ttg aag gga gac ggg atc ctc atc gtc gtc aac aca	305
Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
60 65 70	
gtg ggt gct gcg ctt cag acc ctg tat atc ttg gca tat ctg cat tac	353
Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
75 80 85 90	
tgc cct cgg aag cgt gtt gtg ctc cta cag act gca acc ctg cta ggc	401
Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
95 100 105	
gtc ctt ctc ctg ggt tat ggc tac ttt tgg ctc ctg gta ccc aac cct	449
Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
110 115 120	
gag gcc cgg ctt cag cag ttg ggc ctc ttc tgc agt gtc ttc acc atc	497
Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
125 130 135	
agc atg tac ctc tca cca ctg gct gac ttg gct aag gtg att caa act	545
Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
140 145 150	
aaa tca acc caa tgt ctc tcc tac cca ctc acc att gct acc ctt ctc	593
Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
155 160 165 170	
acc tct gcc tcc tgg tgc ctc tat ggg ttt cga ctc aga gat ccc tat	641
Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	
175 180 185	
atc atg gtg tcc aac ttt cca gga atc gtc acc agc ttt atc cgc ttc	689
Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe	
190 195 200	
tgg ctt ttc tgg aag tac ccc cag gag caa gac agg aac tac tgg ctc	737
Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu	
205 210 215	
ctg caa acc tga ggctgctcat ctgaccactg ggcaccttag tgccaacctg	789
Leu Gln Thr *	
220	
aaccaaagag acctccttgt ttcagctggg cctgctgtcc agcttcccag gtgcagtgagg	849
ttgtgggaac aagagatgac tttgaggata aaaggaccaa agaaaaagct ttacttagat	909
gattgattgg ggcctaggag atgaaatcac tttttatattt ttagagattt ttttttttaa	969
ttttggagggt tggggtgcaa tctttagaat atgccttaaa aggccgggag cggtgggtca	1029
cgctgtaat cccagcactt tgggaggcca aggtgggagc atcgctgag gtcaggagtt	1089

caagaccaac ctgactaaca tgggtgaaacc ccatctctac taaaaataca aaattagcca 1149
 ggcattgatgg cacatgcctg taatcccaga tactttgggag gctgaggcag gagaattgct 1209
 tgaacccagg aggtggaggt tgcagtggagc tgagatcgtg ccattgtgat atgaatatgc 1269
 cttatatgct gatatgaata tgccttaaaa taaagtgttc cccaccctg ccc 1322

<210> 42
 <211> 3045
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (191)...(946)

<400> 42
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 ccgccttctg catcgcggtc tcggcggtt ccacctagac acctaacagt cgcggagccg 120
 gccgcgtcgt gagggggctg gcacggggag tcgggcggtc ttgtgcatct tggctacctg 180
 tgggtcgaag atg tcg gac atc gga gac tgg ttc agg agc atc ccg gcg 229
 Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala
 1 5 10

atc acg cgc tat tgg ttc gcc gcc acc gtc gcc gtg ccc ttg gtc ggc 277
 Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly
 15 20 25

aaa ctc ggc ctc atc agc ccg gcc tac ctc ttc ctc tgg ccc gaa gcc 325
 Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
 30 35 40 45

ttc ctt tat cgc ttt cag att tgg agg cca atc act gcc acc ttt tat 373
 Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr
 50 55 60

ttc cct gtg ggt cca gga act gga ttt ctt tat ttg gtc aat tta tat 421
 Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr
 65 70 75

ttc tta tat cag tat tct acg cga ctt gaa aca gga gct ttt gat ggg 469
 Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly
 80 85 90

agg cca gca gac tat tta ttc atg ctc ctc ttt aac tgg att tgc atc 517
 Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile
 95 100 105

gtg att act ggc tta gca atg gat atg cag ttg ctg atg att cct ctg 565
 Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu
 110 115 120 125

atc atg tca cta ctt tat gtc tgg gcc cag ctg aac aga gac atg att 613
 Ile Met Ser Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile
 130 135 140

gta tca ttt tgg ttt gga aca cga ttt aag gcc tgc tat tta ccc tgg 661
 Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp
 145 150 155

gtt atc ctt gga ttc aac tat atc atc gga ggc tcg gta atc aat gag 709
 Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu
 160 165 170

ctt att gga aat ctg gtt gga cat ctt tat ttt ttc cta atg ttc aga	757
Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg	
175 180 185	
tac cca atg gac ttg gga gga aga aat ttt cta tcc aca cct cag ttt	805
Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe	
190 195 200 205	
ttg tac cgc tgg ctg ccc agt agg aga gga gga gta tca gga ttt ggt	853
Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly	
210 215 220	
gtg ccc cct gct agc atg agg cga gct gct gat cag aat ggc gga ggc	901
Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly	
225 230 235	
ggg aga cac aac tgg ggc cag ggc ttt cga ctt gga gac cag tga	946
Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln *	
240 245 250	
agggggcggcc tcgggcagcc gctcctctca agccacattt cctcccagtg ctgggtgcgc	1006
ttaacaactg cgttcttggt aacactgttg gacctgaccc acactgaatg tagtctttca	1066
gtacgagaca aagtttctta aatcccgaag aaaaatataa gtgttccaca agtttcacga	1126
ttctcattca agtccttact gctgtgaaga acaaatacca actgtgcaaa ttgcaaaact	1186
gactacattt tttggtgtct tctcttctcc cctttccgtc tgaataatgg gtttttagcgg	1246
gtcctagtct gctggcattg agctggggct gggtcaccaa acccttccca aaaggaccct	1306
tatctctttc ttgcacacat gcctctctcc cacttttccc aacccccaca tttgcaacta	1366
gaagagggttg cccataaaat tgctctgccc ttgacagggt ctgttattta ttgacttttg	1426
ccaaggcttg gtcacaacaa tcatattcac gtaattttcc ccctttggtg gcagaactgt	1486
agcaataggg ggagaagaca agcagcggat gaagcggttt ctgagctttt ggaattgctt	1546
cgacctgaca tccgttgtaa ccgtttgcca cttcttcaga tatttttata aaaaagtacc	1606
actgagtcag tgaggggccac agattggtat taatgagata cgagggttgt tgctgggtgt	1666
ttgtttcctg agctaagtga tcaagactgt agtggagttg cagctaacat gggttagggt	1726
taaaccgtgg gggatgcaac ccctttgctt ttcatatgta ggccactagg ctttgtgtag	1786
ctggagtagt tgggttgctt tgtgttagga ggatccagat catgttggt acagggagat	1846
gctctctttg agaggctcct gggcattgat tccatttcaa tctcattctg gatatgtgtt	1906
cattgagtaa aggaggagag accctcatac gctattttaa tgtcactttt ttgcctatcc	1966
cccgtttttt ggtcatgttt caattaattg tgaggaaggc gcagctcctc tctgcacgta	2026
gatcattttt taaagctaata gtaagcacat ctaagggaat aacatgattt aagggtgaaa	2086
tggctttaga atcattttggg tttgagggtg tgttattttg agtcatgaat gtacaagctc	2146
tgtgaatcag accagcttaa ataccacac ctttttttcg taggtgggct tttcctatca	2206
gagcttggtc cataacccaa taaagttttt tgaaggccat ggcttttcac acagtatttt	2266
tattttatga cgttatctga aagcagactg ttaggagcag tattgagtgg ctgtcacact	2326
ttgaggcaac taaaaaggct tcaaacgttt tgatcagttt cttttcagga aacattgtgc	2386
tctaacagta tgactattct ttccccact cttaaacagt gtgatgtgtg ttatcctagg	2446
aaatgagagt tggcaaacaa cttctcattt tgaatagagt ttgtgtgtac ctctccatat	2506
ttaattttata tgataaaata ggtggggaga gtctgaacct taactgtcat gttttgttgt	2566
tcatctgttg ccacaataaa gtttacttgt aaaatttttag aggccattac tccaattatg	2626
ttgcacgtac actcattgta caggcgtgga gactcattgt atgtataaga atattctgac	2686
agtgagtac ccggagtctc tgggtgtacc ctttaccagt cagctgcctg cgagcagtca	2746
ttttttccta aaggtttaca agtatttaga actcttcagt tcagggcaaa atgttcatga	2806
agttattcct cttaaacatg gtttaggaagc tgatgacgtt attgattttg tctggattat	2866
gtttctggaa taattttacc aaaacaagct atttgagttt tgacttgaca aggcaaaaca	2926
tgacagtgga ttctctttac aaattgaaaa aaataatcct tattttgtat aaaggacttc	2986
cctttttgta aactaatcct ttttattggt aaaaattgta aattaaaatg tgcaacttg	3045

<210> 43

<211> 653

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63)...(383)

<400> 43

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atgaccttca cgggaggct gaggtcggag tcccgatttt ctctgctgc tgtggcccgg 60
ac atg gcg act ccc ggc cct gtg att ccg gag gtc ccc ttt gaa cca 107
  Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro
    1             5             10             15

tcg aag cct cca gtc att gag ggg ctg agc ccc act gtt tac agg aat 155
Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn
    20             25             30

cca gag agt ttc aag gaa aag ttc gtt cgc aag acc cgc gag aac ccg 203
Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro
    35             40             45

gtg gta ccc ata ggt tgc ctg gcc acg gcg gcc gcc ctc acc tac ggc 251
Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly
    50             55             60

ctc tac tcc ttc cac cgg ggc aac agc cag cgc tct cag ctc atg atg 299
Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met
    65             70             75

cgc acc cgg atc gcc gcc cag ggt ttc acg gtc gca gcc atc ttg ctg 347
Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu
    80             85             90             95

ggt ctg gct gtc act gct atg aag tct cga ccc taa gcccagggtc 393
Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro *
    100             105

tggccttgaa agctccgcag aaatgattcc aaaacccagg gagcaaccac tggccctacc 453
gtgggactta ctccctctc tcctttgaga ggcccatgtg tcgctgggga ggaagtgacc 513
ctttgtgtaa ctgtaaccga aagttttttc aaaaatccta gatgctgttg tttgaatgtt 573
acatacttct atttgtgcc catctcccct ccaactcccct gcttaataaa ctctaaaaat 633
ccacttgat ttaattcagt 653

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<210> 44

<211> 439

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(311)

<400> 44

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gtagaaacag gcctgttaag gagaggccac cgggacttca gtgtctctc catcccagga 60
gcgcagtggc cact atg ggg tct ggg ctg ccc ctt gtc ctc ctc ttg acc 110
  Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
    1             5             10

ctc ctt ggc agc tca cat gga aca ggg ccg ggt atg act ttg caa ctg 158
Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
    15             20             25

aag ctg aag gag tct ttt ctg aca aat tcc tcc tat gag tcc agc ttc 206

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Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
30 35 40

ctg gaa ttg ctt gaa aag ctc tgc ctc ctc ctc cat ctc cct tca ggg 254
Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
45 50 55 60

acc agc gtc acc ctc cac cat gca aga tct caa cac cat gtt gtc tgc 302
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
65 70 75

aac aca tga cagccattga agcctgtgtc cttcttggcc cgggcttttg 351
Asn Thr *

ggccgggggat gcaggaggca ggccccgacc ctgtcttttca gcaggccccc accctcctga 411
gtggcaataa ataaaattcg gtatgctg 439

<210> 45
<211> 1131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)...(1000)

<400> 45
ctatgagatc ccggcctcag ggtggacgca gtggtttctgc actgaggccc tcgtc atg 58
Met
1

gtg gcg cct gtg tgg tac ttg gta gcg gcg gct ctg cta gtc ggc ttt 106
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
5 10 15

atc ctc ttc ctg act cgc agc cgg ggc cgg gcg gca tca gcc ggc caa 154
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
20 25 30

gag cca ctg cac aat gag gag ctg gca gga gca ggc cgg gtg gcc cag 202
Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln
35 40 45

cct ggg ccc ctg gag cct gag gag ccg aga gct gga ggc agg cct cgg 250
Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg
50 55 60 65

cgc cgg agg gac ctg ggc agc cgc cta cag gcc cag cgt cga gcc cag 298
Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln
70 75 80

cgg gtg gcc tgg gca gaa gca gat gag aac gag gag gaa gct gtc atc 346
Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile
85 90 95

cta gcc cag gag gag gaa ggt gtc gag aag cca gcg gaa act cac ctg 394
Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu
100 105 110

tcg ggg aaa att gga gct aag aaa ctg cgg aag ctg gag gag aaa caa 442

Ser	Gly	Lys	Ile	Gly	Ala	Lys	Lys	Leu	Arg	Lys	Leu	Glu	Glu	Lys	Gln		
115						120					125						
gcg	cga	aag	gcc	cag	cgt	gag	gca	gag	gag	gct	gaa	cgt	gag	gag	cgg	490	
Ala	Arg	Lys	Ala	Gln	Arg	Glu	Ala	Glu	Glu	Ala	Glu	Arg	Glu	Glu	Arg		
130					135					140					145		
aaa	cga	ctc	gag	tcc	cag	cgc	gaa	gct	gag	tgg	aag	aag	gag	gag	gag	538	
Lys	Arg	Leu	Glu	Ser	Gln	Arg	Glu	Ala	Glu	Trp	Lys	Lys	Glu	Glu	Glu		
				150					155					160			
cgg	ctt	cgc	ctg	gag	gag	gag	cag	aag	gag	gag	gag	gag	agg	aag	gcc	586	
Arg	Leu	Arg	Leu	Glu	Glu	Glu	Gln	Lys	Glu	Glu	Glu	Glu	Arg	Lys	Ala		
				165				170					175				
cgc	gag	gag	cag	gcc	cag	cgg	gag	cat	gag	gag	tac	ctg	aaa	ctg	aag	634	
Arg	Glu	Glu	Gln	Ala	Gln	Arg	Glu	His	Glu	Glu	Tyr	Leu	Lys	Leu	Lys		
				180			185					190					
gag	gcc	ttt	gtg	gtg	gag	gag	gaa	ggc	gta	gga	gag	acc	atg	act	gag	682	
Glu	Ala	Phe	Val	Val	Glu	Glu	Glu	Gly	Val	Gly	Glu	Thr	Met	Thr	Glu		
	195					200					205						
gaa	cag	tcc	cag	agc	ttc	ctg	aca	gag	ttc	atc	aac	tac	atc	aag	cag	730	
Glu	Gln	Ser	Gln	Ser	Phe	Leu	Thr	Glu	Phe	Ile	Asn	Tyr	Ile	Lys	Gln		
210					215					220					225		
tcc	aag	gtt	gtg	ctc	ttg	gaa	gac	ctg	gct	tcc	cag	gtg	ggc	cta	cgc	778	
Ser	Lys	Val	Val	Leu	Leu	Glu	Asp	Leu	Ala	Ser	Gln	Val	Gly	Leu	Arg		
				230				235						240			
act	cag	gac	acc	ata	aat	cgc	atc	cag	gac	ctg	ctg	gct	gag	ggg	act	826	
Thr	Gln	Asp	Thr	Ile	Asn	Arg	Ile	Gln	Asp	Leu	Leu	Ala	Glu	Gly	Thr		
			245					250					255				
ata	aca	ggt	gtg	att	gac	gac	cgg	ggc	aag	ttc	atc	tac	ata	acc	cca	874	
Ile	Thr	Gly	Val	Ile	Asp	Asp	Arg	Gly	Lys	Phe	Ile	Tyr	Ile	Thr	Pro		
		260				265						270					
gag	gaa	ctg	gcc	gcc	gtg	gcc	aac	ttc	atc	cga	cag	cgg	ggc	cgg	gtg	922	
Glu	Glu	Leu	Ala	Ala	Val	Ala	Asn	Phe	Ile	Arg	Gln	Arg	Gly	Arg	Val		
	275					280					285						
tcc	atc	gcc	gag	ctt	gcc	caa	gcc	agc	aac	tcc	ctc	atc	gcc	tgg	ggc	970	
Ser	Ile	Ala	Glu	Leu	Ala	Gln	Ala	Ser	Asn	Ser	Leu	Ile	Ala	Trp	Gly		
290					295				300					305			
cgg	gag	tcc	cct	gcc	caa	gcc	cca	gcc	tga	ccccagtcct	tcctctctgg					1020	
Arg	Glu	Ser	Pro	Ala	Gln	Ala	Pro	Ala	*								
				310													
actcagagtt	ggtgtggcct	acctggctat	acatcttcat	ccctcccccac	catcctgggg											1080	
aagtgatggt	gtggccaggc	agttatagat	taaaggcctg	tgagtactgc	t											1131	

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 <213> Homo sapiens

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<222> (79)...(666)

<400> 46

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acctttactc cagagatc atg gct gcc gag gat gtg gtg gcg act ggc gcc 111
                Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala
                    1             5             10

gac cca agc gat ctg gag agc ggc ggg ctg ctg cat gag att ttc acg 159
Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr
                    15             20             25

tcg ccg ctc aac ctg ctg ctg ctt ggc ctc tgc atc ttc ctg ctc tac 207
Ser Pro Leu Asn Leu Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr
                    30             35             40

aag atc gtg cgc ggc gac cag ccg gcg gcc agc ggc gac agc gac gac 255
Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp
                    45             50             55

gac gag ccg ccc cct ctg ccc cgc ctc aag ccg cgc gac ttc acc ccc 303
Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro
                    60             65             70             75

gcc gag ctg ccg cgc ttc gac ggc gtc cag gac ccg cgc ata ctc atg 351
Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met
                    80             85             90

gcc atc aac ggc aag gtg ttc gat gtg acc aaa ggc cgc aaa ttc tac 399
Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr
                    95             100             105

ggg ccc gag ggg ccg tat ggg gtc ttt gct gga aga gat gca tcc agg 447
Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg
                    110             115             120

ggc ctt gcc aca ttt tgc ctg gat aag gaa gca ctg aag gat gag tac 495
Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr
                    125             130             135

gat gac ctt tct gac ctc act gct gcc cag cag gag act ctg agt gac 543
Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp
                    140             145             150             155

tgg gag tct cag ttc act ttc aag tat cat cac gtg ggc aaa ctg ctg 591
Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu
                    160             165             170

aag gag ggg gag gag ccc act gtg tac tca gat gag gaa gaa cca aaa 639
Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys
                    175             180             185

gat gag agt gcc ccg aaa aat gat taa agcattcagt ggaagtatat 686
Asp Glu Ser Ala Arg Lys Asn Asp *
                    190             195

ctatTTTTgt attttgcaaa atcatttgta acagtccact ctgtcttttaa aacatagtga 746
ttacaatatt tagaaagttt tgagcacttg ctataagttt tttataacat cactagtgac 806
actaataaaa ttaacttctt agaatgcatg atgtgtttgt gtgtcacaaa tccagaaagt 866
gaactgcagt gctgtaatac acatgttaat actgtttttc ttctatctgt agttagtaca 926
ggatgaattt aaatgtgttt ttcttgagag acaaggaaga cttgggtatt tcccaaaaca 986

```

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ggtaaaaatc ttaaatgtgc accaagagca aaggatcaac ttttagtcat gatgttctgt 1046
aaagacaaca aatccctttt tttttctcaa ttgacttaac tgcattgattt ctgtttttatc 1106
tacctctaaa gcaaattctgc agtggttccaa agacttttggg atggattaag cgctgtccag 1166
taacaaaaatg aaatctcaaa acagagctca gctgcaaaaa agcatatttt ctgtgtttct 1226
ggactgcact gttgtccttg ccctcacata gacactcaga caccctcaca aacacagtag 1286
tctatagtta ggattaaaat aggatctgaa cattcaaaaag aaagcttttg aaaaaaagag 1346
ctggctggcc taaaaaccta aatatatgat gaagattgta ggactgtctt cccaagcccc 1406
atgttcatgg tggggcaatg gttatttggg tattttactc aattggttac tctcatttga 1466
aatgagggag ggacatacag aataggaaca ggtgtttgct ctcctaagag ccttcatgca 1526
cacccttgaa ccacgaggaa acagtacagt cgctagtcaa gtggttttta aagtaaagta 1586
tattcataag gtaacagtta ttctgttggg ataaaactat acccactgca aaagtagtag 1646
tcaagtgtct aggtctttga tattgtctct ttggttaaca ctaagcttaa gtagactata 1706
cagttgtatg aatttgtaaa agtatatgaa cacctagtga gatttcaaac ttgtaattgt 1766
ggttaaatag tcattgtatt ttcttgtgaa ctgtgtttta tgattttacc tcaaatcaga 1826
aaacaaaatg atgtgctttg gtcagttaat aaaaatgggt ttaccact 1875

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<210> 47

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)...(1460)

<400> 47

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gcggcagaac c atg ttg gac ttc gcg atc ttc gcc gtt acc ttc ttg ctg 110
          Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu
                1             5                 10

```

```

gcg ttg gtg gga gcc gtg ctc tac ctc tat ccg gct tcc aga caa gct 158
Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala
    15             20                 25

```

```

gca gga att cca ggg att act cca act gaa gaa aaa gat ggt aat ctt 206
Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
    30             35                 40                 45

```

```

cca gat att gtg aat agt gga agt ttg cat gag ttc ctg gtt aat ttg 254
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu
                50             55                 60

```

```

cat gag aga tat ggg cct gtg gtc tcc ttc tgg ttt ggc agg cgc ctc 302
His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu
    65             70                 75

```

```

gtg gtt agt ttg ggc act gtt gat gta ctg aag cag cat atc aat ccc 350
Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro
    80             85                 90

```

```

aat aag aca ttg gac cct ttt gaa acc atg ctg aag tca tta tta agg 398
Asn Lys Thr Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg
    95             100                 105

```

```

tat caa tct ggt ggt ggc agt gtg agt gaa aac cac atg agg aaa aaa 446
Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys
110             115                 120                 125

```

```

ttg tat gaa aat ggt gtg act gat tct ctg aag agt aac ttt gcc ctc 494
Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu

```


130										135					140					
ctc	cta	aag	ctt	tca	gaa	gaa	tta	tta	gat	aaa	tgg	ctc	tcc	tac	cca	542				
Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro					
			145					150						155						
gag	acc	cag	cac	gtg	ccc	ctc	agc	cag	cat	atg	ctt	ggg	ttt	gct	atg	590				
Glu	Thr	Gln	His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met					
		160					165					170								
aag	tct	gtt	aca	cag	atg	gta	atg	ggg	agt	aca	ttt	gaa	gat	gat	cag	638				
Lys	Ser	Val	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln					
	175					180					185									
gaa	gtc	att	cgc	ttc	cag	aag	aat	cat	ggc	aca	gtt	tgg	tct	gag	att	686				
Glu	Val	Ile	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile					
190					195					200					205					
gga	aaa	ggc	ttt	cta	gat	ggg	tca	ctt	gat	aaa	aac	atg	act	cgg	aaa	734				
Gly	Lys	Gly	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys					
				210					215					220						
aaa	caa	tat	gaa	gat	gcc	ctc	atg	caa	ctg	gag	tct	gtt	tta	agg	aac	782				
Lys	Gln	Tyr	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn					
			225					230					235							
atc	ata	aaa	gaa	cga	aaa	gga	agg	aac	ttc	agt	caa	cat	att	ttc	att	830				
Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile					
		240					245					250								
gac	tcc	tta	gta	caa	ggg	aac	ctt	aat	gac	caa	cag	atc	cta	gaa	gac	878				
Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp					
	255					260					265									
agt	atg	ata	ttt	tct	ctg	gcc	agt	tgc	ata	ata	act	gca	aaa	ttg	tgt	926				
Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys					
270						275				280					285					
acc	tgg	gca	atc	tgt	ttt	tta	acc	acc	tct	gaa	gaa	gtt	caa	aaa	aaa	974				
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys					
				290					295					300						
tta	tat	gaa	gag	ata	aac	caa	gtt	ttt	gga	aat	ggg	cct	gtt	act	cca	1022				
Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro					
			305					310					315							
gag	aaa	att	gag	cag	ctc	aga	tat	tgt	cag	cat	gtg	ctt	tgt	gaa	act	1070				
Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr					
		320					325					330								
gtt	cga	act	gcc	aaa	ctg	act	cca	gtt	tct	gcc	cag	ctt	caa	gat	att	1118				
Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile					
	335						340				345									
gaa	gga	aaa	att	gac	cga	ttt	att	att	cct	aga	gag	acc	ctc	gtc	ctt	1166				
Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu					
350					355				360						365					
tat	gcc	ctt	ggg	gtg	gta	ctt	cag	gat	cct	aat	act	tgg	cca	tct	cca	1214				
Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro					
				370					375					380						

```

cac aag ttt gat cca gat cgg ttt gat gat gaa tta gta atg aaa act 1262
His Lys Phe Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr
                               385                               395

ttt tcc tca ctt gga ttc tca ggc aca cag gag tgt cca gag ttg agg 1310
Phe Ser Ser Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg
                               400                               410

ttt gca tat atg gtg acc aca gta ctt ctt agt gta ttg gtg aag aga 1358
Phe Ala Tyr Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg
                               415                               425

ctg cac cta ctt tct gtg gag gga cag gtt att gaa aca aag tat gaa 1406
Leu His Leu Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu
430                               435                               440                               445

ctg gta aca tca tca agg gaa gaa gct tgg atc act gtc tca aag aga 1454
Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg
                               450                               455                               460

tat taa aattttatac atttaaaatc attgttaaatt tgattgagga aacaaccatt 1510
Tyr *

taaaaaaaaaat ctatgttgaa tcctttttata aaccagtatc actttgtaat at 1562

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<220>
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<222> (171)...(914)

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gcgccccctcg tggggtcgcg ttgccacccc acgcgggactc cccagctggc gcgccccctcc 120
catttgccctg tcctggtcag gccccacccc cccttcccac ctgaccagcc atg ggg 176
                                                Met Gly
                                                1

gct gcg gtg ttt ttc ggc tgc act ttc gtc gcg ttc ggc ccg gcc ttc 224
Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe
                               5                               10                               15

gcg ctt ttc ttg atc act gtg gct ggg gac ccg ctt cgc gtt atc atc 272
Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val Ile Ile
                               20                               25                               30

ctg gtc gca ggg gca ttt ttc tgg ctg gtc tcc ctg ctc ctg gcc tct 320
Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu Ala Ser
35                               40                               45                               50

gtg gtc tgg ttc atc ttg gtc cat gtg acc gac ccg tca gat gcc cgg 368
Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp Ala Arg
                               55                               60                               65

ctc cag tac ggc ctc ctg att ttt ggt gct gct gtc tct gtc ctt cta 416
Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val Leu Leu

```

70	75	80	
cag gag gtg ttc cgc ttt gcc tac tac aag ctg ctt aag aag gca gat			464
Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys Ala Asp			
85	90	95	
gag ggg tta gca tcg ctg agt gag gac gga aga tca ccc atc tcc atc			512
Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile Ser Ile			
100	105	110	
cgc cag atg gcc tat gtt tct ggt ctc tcc ttc ggt atc atc agt ggt			560
Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly			
115	120	125	130
gtc ttc tct gtt atc aat att ttg gct gat gca ctt ggg cca ggt gtg			608
Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val			
135	140	145	
gtt ggg atc cat gga gac tca ccc tat tac ttc ctg act tca gcc ttt			656
Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe			
150	155	160	
ctg aca gca gcc att atc ctg ctc cat acc ttt tgg gga gtt gtg ttc			704
Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe			
165	170	175	
ttt gat gcc tgt gag agg aga cgg tac tgg gct ttg ggc ctg gtg gtt			752
Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu Val Val			
180	185	190	
ggg agt cac cta ctg aca tcg gga ctg aca ttc ctg aac ccc tgg tat			800
Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr			
195	200	205	210
gag gcc agc ctg ctg ccc atc tat gca gtc act gtt tcc atg ggg ctc			848
Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly Leu			
215	220	225	
tgg gcc ttc atc aca gct gga ggg tcc ctc cga agt att cag cgc agc			896
Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser			
230	235	240	
ctc ttg tgt aag gac tga ctacctggac tgatcgccctg acagatccca			944
Leu Leu Cys Lys Asp *			
245			
cctgcctgtc cactgcccatt gactgagccc agccccagcc cgggtccatt gccacattc			1004
tctgtctcct tctcgtcggc ctaccccaact acctccaggg ttttgctttg tcctttttgtg			1064
accgttagtc tctaagcttt accaggagca gcctgggttc agccagtcag tgactgggtg			1124
gtttgaatct gcacttatcc ccaccacctg gggacccctt tgttgtgtcc aggactcccc			1184
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gagggaaacct aggggggacc cctgggcctg ggggtgccctc ctgatgtcct cgccctgtat			1364
ttctccatct ccagtctctg acagtgcagg ttgccaaagaa aaggggaccta gtttagccat			1424
tgcctggag atgaaattaa tggaggctca aggatagatg agctctgagt ttctcagtac			1484
tcctcaaga ctggacatct tggctctttt ctcaggcctg agggggaacc atttttggtg			1544
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ttggaactct tctaacctcc ttgggctata ttttctctcc tcgagttgct cctcatggct			1664
gggctcattt cggctccctt ctccttggtc ccagaccttg ggggaaagga aggaagtgca			1724
tgtttgggaa ctggcattac tggaactaat ggttttaacc tccttaacca ccagcatccc			1784
tcctctcccc aaggtgaagt ggagggtgct gtggtgagct ggccactcca gagctgcagt			1844

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gccactggag gagtcagact accatgacat cgtaggggaag gaggggagat ttttttgtag 1904
tttttaattg ggggtgtgga ggggcgggga gggtttctat aaactgtatc attttctgct 1964
gaggggtggag tgtcccatcc ttttaaatcaa ggtgattgtg attttgacta ataaaaaaga 2024
atttgt 2030
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<210> 49
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<220>
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 <222> (98)...(439)

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tccgtcccgga gaaggagaa gaggccgaag aggaaac atg aac ttc tat tta ctc 115
Met Asn Phe Tyr Leu Leu
1 5
```

```
cta gcg agc agc att ctg tgt gcc ttg att gtc ttc tgg aaa tat cgc 163
Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg
10 15 20
```

```
cgc ttt cag aga aac act ggc gaa atg tca tca aat tca act gct ctt 211
Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
25 30 35
```

```
gca cta gtg aga ccc tct tct tct ggg tta att aac agc aat aca gac 259
Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
40 45 50
```

```
aac aat ctt gca gtc tac gac ctc tct cgg gat att tta aat aat ttc 307
Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
55 60 65 70
```

```
cca cac tca ata gcc agg cag aag cga ata ttg gta aac ctc agt atg 355
Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
75 80 85
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```
gtg gaa aac aag ctg gtt gaa ctg gaa cat act cta ctt agc aag ggt 403
Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
90 95 100
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ttc aga ggt cca tca cct cac cgg aaa tcc acc taa aagcgtacag 449
Phe Arg Gly Pro Ser Pro His Arg Lys Ser Thr *
105 110
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gatgtaatgc cagtgggtgga aatcattaaa gacactttga gtag 493
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ggctctgctg atggttccga atcatggagc tgcagagagc tcctccagcc tggagacggt 180
cttggtgaaa gctgtggtct aactccaccg gctcttcctg cacattgtat tcaagagggg 240
tgctgcccc cgctgactca ggagctccgg tgctgcagcc gccacga atg ggg agg 296
                                     Met Gly Arg
                                     1

tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg gtg ttg acc ctg ggg 344
Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly
      5                                10                                15

ctg gtg ctt ctc tac tac tgc ttc tcc atc ggc atc acc ttc tac aac 392
Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn
  20                                25                                30                                35

aag tgg ctg aca aag agc ttc cat ttc ccc ctc ttc atg acg atg ctg 440
Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu
                        40                                45                                50

cac ctg gcc gtg atc ttc ctc ttc tcc gcc ctg tcc agg gcg ctg gtt 488
His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg Ala Leu Val
                        55                                60                                65

cag tgc tcc agc cac agg gcc cgt gtg gtg ctg agc tgg gcc gac tac 536
Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp Ala Asp Tyr
      70                                75                                80

ctc aga aga gtg gct ccc aca gct ctg gcg acg gcg ctt gac gtg ggc 584
Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu Asp Val Gly
      85                                90                                95

ttg tcc aac tgg agc ttc ctg tat gtc acc gtc tcg ctg tac aca atg 632
Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu Tyr Thr Met
  100                                105                                110                                115

acc aaa tcc tca gct gtc ctc ttc atc ttg atc ttc tct ctg atc ttc 680
Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser Leu Ile Phe
                        120                                125                                130

aag ctg gag gag ctg cgc gcg gca ctg gtc ctg gtg gtc ctc ctc atc 728
Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val Leu Leu Ile
      135                                140                                145

gcc ggg ggt ctc ttc atg ttc acc tac aag tcc aca cag ttc aac gtg 776
Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln Phe Asn Val
      150                                155                                160

gag ggc ttc gcc ttg gtg ctg ggg gcc tcg ttc atc ggt ggc att cgc 824
Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly Gly Ile Arg
      165                                170                                175

tgg acc ctc acc cag atg ctc ctg cag aag gct gaa ctc ggc ctc cag 872
Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu Gly Leu Gln
  180                                185                                190                                195

aat ccc atc gac acc atg ttc cac ctg cag cca ctc atg ttc ctg ggg 920
Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met Phe Leu Gly
                        200                                205                                210

ctc ttc cct ctc ttt gct gta ttt gaa ggt ctc cat ttg tcc aca tct 968
Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu Ser Thr Ser

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215	220	225	
gag aaa atc ttc cgt ttc cag gac aca ggg ctg ctc ctg cgg gta ctt			1016
Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu Arg Val Leu			
230	235	240	
ggg agc ctc ttc ctt ggc ggg att ctc gcc ttt ggt ttg ggc ttc tct			1064
Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu Gly Phe Ser			
245	250	255	
gag ttc ctc ctg gtc tcc aga acc tcc agc ctc act ctc tcc att gcc			1112
Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu Ser Ile Ala			
260	265	270	275
ggc att ttt aag gaa gtc tgc act ttg ctg ttg gca gct cat ctg ctg			1160
Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu			
280	285	290	
ggc gat cag atc agc ctc ctg aac tgg ctg ggc ttc gcc ctc tgc ctc			1208
Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu			
295	300	305	
tcg gga ata tcc ctc cac gtt gcc ctc aaa gcc ctg cat tcc aga ggt			1256
Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly			
310	315	320	
gat ggt ggc ccc aag gcc ttg aag ggg ctg ggc tcc agc ccc gac ctg			1304
Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu			
325	330	335	
gag ctg ctg ctc cgg agc agc cag cgg gag gaa ggt gac aat gag gag			1352
Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu			
340	345	350	355
gag gag tac ttt gtg gcc cag ggg cag cag tga ccagccaggg caaatggctt			1405
Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln *			
360	365		
agaagcaggc cactccccag cctgctgcca gcaactcactg tgctcaagcc gccagggctc			1465
atcatggtag ctgggagctg tggacgggag tcaccagggtg gtggggccaa gccagggact			1525
catgactttt gcccctccct tcagagcctg gtcacacaag gggcgagcac caggccagcc			1585
tgggactggc cagagctggg cccaagctgc gctggaatcg cagcaggaga ggggagtggg			1645
ctgtttcttc ccaccacttc ccaggctctg acagccgaga ctcatttcca aggcacagca			1705
gctttctaaa gggactgagt ttggactggg ttttggacct ccaggggctg gagcttcac			1765
acctgggcag tgtcttttct cagagagcag gtttctttat agtttggaaa taaatggttc			1825
acggtccact ggccgccttg tgttgctgga gacgtggggg caggagggg acagtgtggg			1885
cctggcctct cctttccttt ccctgcctgg agccttcttc aaatgtctgg tcttaagcca			1945
ggcctccttc attttctcgc tcctgttaga acaccagtcc cctccccagt ggggccccac			2005
tgcacctgct ggcaggaaat aaatgaatgt ttactgagt			2044
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tccattttcta aataccagac ttcaaaagat aaggttcaaa agtggttataa gaagatattc	120
ctttttttgt cctagagaac ttatttttct gtgaaa atg cct acc aca aag aag	174
Met Pro Thr Thr Lys Lys	
1 5	
aca ttg atg ttc tta tca agc ttt ttc acc agc ctt ggg tcc ttc att	222
Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile	
10 15 20	
gta att tgc tct att ctt ggg aca caa gca tgg atc acc agt aca att	270
Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile	
25 30 35	
gct gtt aga gac tct gct tca aat ggg agc att ttc atc act tac gga	318
Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly	
40 45 50	
ctt ttt cgt ggg gag agt agt gaa gaa ttg agt cac gga ctt gca gaa	366
Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu	
55 60 65 70	
cca aag aaa aag ttt gca gtt tta gag ata ctg aat aat tct tcc caa	414
Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln	
75 80 85	
aaa act ctg cat tcg gtg act atc ctg ttc ctg gtc ctg agt ttg atc	462
Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile	
90 95 100	
acg tcg ctg ctg agc tct ggg ttt acc ttc tac aac agc atc agc aac	510
Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn	
105 110 115	
cct tac cag aca ttc ctg ggg ccg acg ggg gtg tac acc tgg aac ggg	558
Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
120 125 130	
ctc ggt gca tcc ttc gtt ttt gtg acc atg ata ctg ttt gtg gcg aac	606
Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
135 140 145 150	
acg cag tcc aac caa ctc tcc gaa gag ttg ttc caa atg ctt tac ccg	654
Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
155 160 165	
gca acc acc agt aaa gga acg acc cac agt tac gga tac tcg ttc tgg	702
Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
170 175 180	
ctc ata ctg ctc gtc att ctt cta aat ata gtc act gta acc atc atc	750
Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
185 190 195	
att ttc tac cag aag gcc aga tac cag cgg aag cag gag cag aga aag	798
Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
200 205 210	
cca atg gaa tat gct cca agg gac gga att tta ttc tga attctcttttc	847
Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe *	
215 220 225	

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 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
 1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
 15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207
 Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255
 Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
 50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303
 Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
 65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351
 Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
 80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg ggc tct gag gac aaa 399
 Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
 95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447
 Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
 110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495
 Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
 130 135 140

ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543
 Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
 145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594
 Lys Ala Leu Pro Arg Ser *
 160

accgctgccg gtggtaacca gtggaagacc ccagccccca gggagaggac cccgttctat 654
 cccagccat gataataaag ctgctctccc agctgcctct c 695

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<220>

<221> CDS

<222> (80)...(661)

<400> 54

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          Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys
                1                5                10

cgc tgg atc ctg ccc ctg ctc cta ctc agc gcc atc gcc ttc gac atc 160
Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile
          15                20                25

atc gcg ctg gcc ggc cgc ggc tgg ttg cag tct agc gac cac ggc cag 208
Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln
          30                35                40

acg tcc tcg ctg tgg tgg aaa tgc tcc caa gag ggc ggc ggc agc ggg 256
Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly
          45                50                55

tcc tac gag gag ggc tgt cag agc ctc atg gag tac gcg tgg ggt aga 304
Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg
          60                65                70                75

gca gcg gct gcc atg ctc ttc tgt ggc ttc atc atc ctg gtg atc tgt 352
Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys
          80                85                90

ttc atc ctc tcc ttc ttc gcc ctc tgt gga ccc cag atg ctt gtc ttc 400
Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe
          95                100                105

ctg aga gtg att gga ggt ctc ctt gcc ttg gct gct gtg ttc cag atc 448
Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile
          110                115                120

atc tcc ctg gta att tac ccc gtg aag tac acc cag acc ttc acc ctt 496
Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu
          125                130                135

cat gcc aac cgt gct gtc act tac atc tat aac tgg gcc tac ggc ttt 544
His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe
          140                145                150                155

ggg tgg gca gcc acg att atc ctg atc ggc tgt gcc ttc ttc ttc tgc 592
Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys
          160                165                170

tgc ctc ccc aac tac gaa gat gac ctt ctg ggc aat gcc aag ccc agg 640
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg
          175                180                185

tac ttc tac aca tct gcc taa cttgggaatg aatgtgggag aaaatcgctg 691
Tyr Phe Tyr Thr Ser Ala *
          190

ctgctgagat ggactccaga agaagaaact gtttctccag gcgactttga acccattttt 751

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tggcagtgtt catattatta aactagtcaa ataagctaaa ataatttggg agaaaatatt 811
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ttcactaatt acctatacta tgccaatatt tccttatatc tatccataac atttatacta 931
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gataggatcat tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttta 1831
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tttccaata aaccaggtat tct 1914

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20

<210> 56
 <211> 16
 <212> DNA
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<400> 56
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16

<210> 57
 <211> 367
 <212> PRT
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<400> 57
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 His Ser Ala Pro His Gly Pro Gly Leu Ile Tyr Arg Gln Pro Asn Cys
 20 25 30
 Asp Asp Pro Glu Thr Glu Glu Ala Ala Leu Val Ala Ile Asp Tyr Ile
 35 40 45
 Asn Gln Asn Leu Pro Trp Gly Tyr Lys His Thr Leu Asn Gln Ile Asp
 50 55 60
 Glu Val Lys Val Trp Pro Gln Gln Pro Ser Gly Glu Leu Phe Glu Ile
 65 70 75 80
 Glu Ile Asp Thr Leu Glu Thr Thr Cys His Val Leu Asp Pro Thr Pro
 85 90 95
 Val Ala Arg Cys Ser Val Arg Gln Leu Lys Glu His Ala Val Glu Gly
 100 105 110
 Asp Cys Asp Phe Gln Leu Leu Lys Leu Asp Gly Lys Phe Ser Val Val
 115 120 125
 Tyr Ala Lys Cys Asp Ser Ser Pro Asp Ser Ala Glu Asp Val Arg Lys
 130 135 140

Val	Cys	Gln	Asp	Cys	Pro	Leu	Leu	Ala	Pro	Leu	Asn	Asp	Thr	Arg	Val
145					150					155					160
Val	His	Ala	Ala	Lys	Ala	Ala	Leu	Ala	Ala	Phe	Asn	Ala	Gln	Asn	Asn
				165						170					175
Gly	Ser	Asn	Phe	Gln	Leu	Glu	Glu	Ile	Ser	Arg	Ala	Gln	Leu	Val	Pro
			180					185					190		
Leu	Pro	Pro	Ser	Thr	Tyr	Val	Glu	Phe	Thr	Val	Ser	Gly	Thr	Asp	Cys
		195					200					205			
Val	Ala	Lys	Glu	Ala	Thr	Glu	Ala	Ala	Lys	Cys	Asn	Leu	Leu	Ala	Glu
	210					215					220				
Lys	Gln	Tyr	Gly	Phe	Cys	Lys	Ala	Thr	Leu	Ser	Glu	Lys	Leu	Gly	Gly
225					230					235					240
Ala	Glu	Val	Ala	Val	Thr	Cys	Thr	Val	Phe	Gln	Thr	Gln	Pro	Val	Thr
				245					250					255	
Ser	Gln	Pro	Gln	Pro	Glu	Gly	Ala	Asn	Glu	Ala	Val	Pro	Thr	Pro	Val
			260					265					270		
Val	Asp	Pro	Asp	Ala	Pro	Pro	Ser	Pro	Pro	Leu	Gly	Ala	Pro	Gly	Leu
	275						280					285			
Pro	Pro	Ala	Gly	Ser	Pro	Pro	Asp	Ser	His	Val	Leu	Leu	Ala	Ala	Pro
	290					295					300				
Pro	Gly	His	Gln	Leu	His	Arg	Ala	His	Tyr	Asp	Leu	Arg	His	Thr	Phe
305					310					315					320
Met	Gly	Val	Val	Ser	Leu	Gly	Ser	Pro	Ser	Gly	Glu	Val	Ser	His	Pro
				325					330					335	
Arg	Lys	Thr	Arg	Thr	Val	Val	Gln	Pro	Ser	Val	Gly	Ala	Ala	Ala	Gly
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 <212> PRT
 <213> Rattus rattus

<400> 58

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			20					25					30		
Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Leu	Ala	Arg	Gln
			35				40					45			
Leu	Asp	Arg	Arg	Gly	Met	Arg	Val	Leu	Ala	Ala	Cys	Leu	Thr	Glu	Lys
	50				55						60				
Gly	Ala	Glu	Gln	Leu	Arg	Ser	Lys	Thr	Ser	Asp	Arg	Leu	Glu	Thr	Val
65					70					75					80
Ile	Leu	Asp	Val	Thr	Lys	Thr	Glu	Ser	Ile	Val	Ala	Ala	Thr	Gln	Trp
				85					90					95	
Val	Lys	Glu	Arg	Val	Gly	Asn	Arg	Gly	Leu	Trp	Gly	Leu	Val	Asn	Asn
			100					105					110		
Ala	Gly	Ile	Ser	Val	Pro	Val	Gly	Pro	Asn	Glu	Trp	Met	Arg	Lys	Lys
		115					120					125			
Asp	Phe	Ala	Ser	Val	Leu	Asp	Val	Asn	Leu	Leu	Gly	Val	Ile	Glu	Val
	130					135					140				
Thr	Leu	Asn	Met	Leu	Pro	Leu	Val	Arg	Lys	Ala	Arg	Gly	Arg	Val	Val
145					150					155					160
Asn	Ile	Ala	Ser	Thr	Met	Gly	Arg	Met	Ser	Leu	Val	Gly	Gly	Gly	Tyr
				165					170					175	
Cys	Ile	Ser	Lys	Tyr	Gly	Val	Glu	Ala	Phe	Ser	Asp	Ser	Leu	Arg	Arg
			180					185					190		
Glu	Leu	Thr	Tyr	Phe	Gly	Val	Lys	Val	Ala	Ile	Ile	Glu	Pro	Gly	Gly

	195		200		205										
Phe	Lys	Thr	Asn	Val	Thr	Asn	Met	Glu	Arg	Leu	Ser	Asp	Asn	Leu	Lys
	210					215						220			
Lys	Leu	Trp	Asp	Gln	Thr	Thr	Glu	Glu	Val	Lys	Glu	Ile	Tyr	Gly	Glu
	225					230					235				240
Lys	Phe	Gln	Asp	Ser	Tyr	Met	Lys	Ala	Met	Glu	Ser	Leu	Val	Asn	Thr
				245					250					255	
Cys	Ser	Gly	Asp	Leu	Ser	Leu	Val	Thr	Asp	Cys	Met	Glu	His	Ala	Leu
			260					265					270		
Thr	Ser	Cys	His	Pro	Arg	Thr	Arg	Tyr	Ser	Pro	Gly	Trp	Asp	Ala	Lys
		275					280					285			
Phe	Phe	Tyr	Leu	Pro	Met	Ser	Tyr	Leu	Pro	Thr	Phe	Leu	Ser	Asp	Ala
	290					295					300				
Val	Ile	His	Trp	Gly	Ser	Val	Lys	Pro	Ala	Arg	Ala	Leu			
305					310					315					

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 <212> PRT
 <213> Homo Sapiens

<400> 59

Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Leu	Gln	Gln	Leu	Gly	Leu	Leu	Glu
1				5					10					15	
Glu	Glu	Gln	Leu	Arg	Gly	Leu	Gly	Phe	Arg	Gln	Thr	Arg	Gly	Tyr	Lys
			20					25					30		
Ser	Leu	Ala	Gly	Cys	Leu	Gly	His	Gly	Pro	Leu	Val	Leu	Gln	Leu	Leu
		35					40					45			
Ser	Phe	Thr	Leu	Leu	Ala	Gly	Leu	Leu	Val	Gln	Val	Ser	Lys	Val	Pro
	50					55					60				
Ser	Ser	Ile	Ser	Gln	Glu	Gln	Ser	Arg	Gln	Asp	Ala	Ile	Tyr	Gln	Asn
	65			70					75					80	
Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys
			85					90					95		
Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly
		100					105					110			
Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr
	115					120					125				
Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln
	130					135					140				
Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Trp	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu
	145			150				155						160	
Pro	Glu	Lys	Ser	Lys	Met	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu
			165				170						175		
Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile
		180					185					190			
Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu
	195					200					205				
Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala
	210					215					220				
Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Glu	Ile	Tyr	Gln	
	225			230						235				240	
Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Glu	Arg	Leu	Cys	His	Pro	Cys
			245					250					255		
Pro	Trp	Glu	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn
		260					265					270			
Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Ile	Thr	Ala	Cys	Lys	Glu	Val	Gly
	275					280					285				
Ala	Gln	Leu	Val	Val	Ile	Lys	Ser	Ala	Glu	Glu	Gln	Asn	Phe	Leu	Gln
	290					295					300				

Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
 305 310 315 320
 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
 325 330 335
 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
 340 345 350
 Glu Glu Asp Cys
 355

<210> 60
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(23)
 <223> Xaa = Any Amino Acid

<400> 60
 Ile Tyr Gln Xaa Leu Thr Xaa Leu Lys Ala Ala Val Gly Glu Leu Xaa
 1 5 10 15
 Xaa Xaa Ser Lys Xaa Gln Xaa
 20

<210> 61
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 61
 Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser Leu Val Gly
 1 5 10 15
 Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr Phe Pro Asn
 20 25 30
 Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
 35 40 45
 Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
 50 55 60
 Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
 65 70 75 80
 His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
 85 90 95
 Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
 100 105 110
 Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
 115 120 125
 Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser
 130 135 140
 Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val
 145 150 155 160
 Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu
 165 170 175
 Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe
 180 185 190
 Cys Cys Ser His Gln Gln Gln Tyr Asp Cys
 195 200

<210> 62
 <211> 221
 <212> PRT
 <213> Mus musculus

<400> 62
 Met Glu Ala Gly Gly Val Ala Asp Ser Phe Leu Ser Ser Ala Cys Val
 1 5 10 15
 Leu Phe Thr Leu Gly Met Phe Ser Thr Gly Leu Ser Asp Leu Arg His
 20 25 30
 Met Gln Arg Thr Arg Ser Val Asp Asn Ile Gln Phe Leu Pro Phe Leu
 35 40 45
 Thr Thr Asp Val Asn Asn Leu Ser Trp Leu Ser Tyr Gly Val Leu Lys
 50 55 60
 Gly Asp Gly Thr Leu Ile Ile Val Asn Ser Val Gly Ala Val Leu Gln
 65 70 75 80
 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Ser Pro Gln Lys His Gly
 85 90 95
 Val Leu Leu Gln Thr Ala Thr Leu Leu Ala Val Leu Leu Leu Gly Tyr
 100 105 110
 Gly Tyr Phe Trp Leu Leu Val Pro Asp Leu Glu Ala Arg Leu Gln Gln
 115 120 125
 Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
 130 135 140
 Leu Ala Asp Leu Ala Lys Ile Val Gln Thr Lys Ser Thr Gln Arg Leu
 145 150 155 160
 Ser Phe Ser Leu Thr Ile Ala Thr Leu Phe Cys Ser Ala Ser Trp Ser
 165 170 175
 Ile Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Ala Val Pro Asn Leu
 180 185 190
 Pro Gly Ile Leu Thr Ser Leu Ile Arg Leu Gly Leu Phe Cys Lys Tyr
 195 200 205
 Pro Pro Glu Gln Asp Arg Lys Tyr Arg Leu Leu Gln Thr
 210 215 220

<210> 63
 <211> 245
 <212> PRT
 <213> Cephalobidae elegans

<400> 63
 Met Asp Leu Glu Asn Phe Leu Leu Gly Ile Pro Ile Val Thr Arg Tyr
 1 5 10 15
 Trp Phe Leu Ala Ser Thr Ile Ile Pro Leu Leu Gly Arg Phe Gly Phe
 20 25 30
 Ile Asn Val Gln Trp Met Phe Leu Gln Trp Asp Leu Val Val Asn Lys
 35 40 45
 Phe Gln Phe Trp Arg Pro Leu Thr Ala Leu Ile Tyr Tyr Pro Val Thr
 50 55 60
 Pro Gln Thr Gly Phe His Trp Leu Met Met Cys Tyr Phe Leu Tyr Asn
 65 70 75 80
 Tyr Ser Lys Ala Leu Glu Ser Glu Thr Tyr Arg Gly Arg Ser Ala Asp
 85 90 95
 Tyr Leu Phe Met Leu Ile Phe Asn Trp Phe Phe Cys Ser Gly Leu Cys
 100 105 110
 Met Ala Leu Asp Ile Tyr Phe Leu Leu Glu Pro Met Val Ile Ser Val
 115 120 125
 Leu Tyr Val Trp Cys Gln Val Asn Lys Asp Thr Ile Val Ser Phe Trp
 130 135 140
 Phe Gly Met Arg Phe Pro Ala Arg Tyr Leu Pro Trp Val Leu Trp Gly

145					150					155					160
Phe	Asn	Ala	Val	Leu	Arg	Gly	Gly	Gly	Thr	Asn	Glu	Leu	Val	Gly	Ile
				165					170					175	
Leu	Val	Gly	His	Ala	Tyr	Phe	Phe	Val	Ala	Leu	Lys	Tyr	Pro	Asp	Glu
				180					185					190	
Tyr	Gly	Val	Asp	Leu	Ile	Ser	Thr	Pro	Glu	Phe	Leu	His	Arg	Leu	Ile
				195					200					205	
Pro	Asp	Glu	Asp	Gly	Gly	Ile	His	Gly	Gln	Asp	Gly	Asn	Ile	Arg	Gly
				210					215					220	
Ala	Arg	Gln	Gln	Pro	Arg	Gly	His	Gln	Trp	Pro	Gly	Gly	Val	Gly	Ala
225					230					235					240
Arg	Leu	Gly	Gly	Asn											
				245											

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<210> 64
<211> 241
<212> PRT
<213> Cephalobidae elegans
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[illegible]

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<210> 65
<211> 239
<212> PRT
<213> Sus scrofa
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<400> 65


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Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
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Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
20      25      30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35      40      45
Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Met Ala Ala Glu
50      55      60
Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu Glu Gly Gly Gly
65      70      75      80
Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu Leu Leu Leu Gly
85      90      95
Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly Asp Gln Pro Ala
100     105     110
Ala Ser Asp Ser Asp Asp Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys
115     120     125
Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe Asp Gly Val Gln
130     135     140
Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val Phe Asp Val Thr
145     150     155     160
Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala
165     170     175
Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu
180     185     190
Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu Thr Pro Ala Gln
195     200     205
Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr Phe Lys Tyr His
210     215     220
His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro Thr Val Tyr
225     230     235

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<210> 66
 <211> 499
 <212> PRT
 <213> Macaca fascicularis

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<400> 66
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1      5      10      15
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
20      25      30
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
35      40      45
Val Asn Ser Gly Ser Leu His Glu Phe Met Asp Leu Ile Pro Asp Leu
50      55      60
Ala Val Glu Thr Trp Leu Leu Leu Ala Val Thr Leu Val Leu Leu Tyr
65      70      75      80
Leu Tyr Gly Thr His Ser His Gly Leu Phe Lys Lys Leu Gly Ile Pro
85      90      95
Gly Pro Thr Pro Leu Pro Leu Leu Gly Asn Ile Leu Ser Tyr Arg Lys
100     105     110
Gly Phe Trp Thr Asp Met Glu Cys Tyr Lys Lys Tyr Gly Lys Val Trp
115     120     125
Gly Phe Tyr Asp Gly Arg Gln Pro Val Leu Ala Ile Thr Asp Pro Asn
130     135     140
Met Ile Lys Thr Val Leu Val Lys Glu Cys Tyr Ser Val Phe Thr Asn
145     150     155     160
Arg Arg Pro Phe Gly Pro Val Gly Phe Met Lys Asn Ala Ile Ser Ile
165     170     175
Ala Glu Asp Glu Glu Trp Lys Arg Ile Arg Ser Leu Leu Ser Pro Thr

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<210> 67
<211> 457
<212> PRT
<213> Saccharomyces cerevisiae
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<400> 67															
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Thr	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Tyr	Cys	Phe	Ser	Ile	Gly	Ile	Thr
			20					25					30		
Phe	Tyr	Asn	Lys	Trp	Leu	Thr	Lys	Ser	Phe	His	Phe	Pro	Leu	Phe	Met
		35					40					45			
Thr	Met	Leu	His	Leu	Ala	Met	Asn	Arg	Thr	Val	Phe	Leu	Ala	Phe	Val
	50					55					60				
Phe	Gly	Trp	Tyr	Phe	Cys	Ser	Ile	Ala	Leu	Ser	Ile	Tyr	Asn	Arg	Trp
65					70					75				80	
Met	Phe	Asp	Pro	Lys	Asp	Gly	Leu	Gly	Ile	Gly	Tyr	Pro	Val	Leu	Val
				85					90					95	

Thr	Thr	Phe	His	Gln	Ala	Thr	Leu	Trp	Leu	Leu	Ser	Gly	Ile	Tyr	Ile		
			100					105					110				
Lys	Leu	Arg	His	Lys	Pro	Val	Lys	Asn	Val	Leu	Arg	Lys	Asn	Asn	Gly		
		115					120					125					
Phe	Asn	Trp	Ser	Phe	Phe	Leu	Lys	Phe	Leu	Leu	Pro	Thr	Ala	Val	Ala		
	130					135					140						
Ser	Ala	Gly	Asp	Ile	Gly	Leu	Ser	Asn	Val	Ser	Phe	Gln	Tyr	Val	Pro		
145					150					155					160		
Leu	Thr	Ile	Tyr	Thr	Ile	Ile	Lys	Ser	Ser	Ser	Ile	Ala	Phe	Val	Leu		
				165					170						175		
Leu	Phe	Gly	Cys	Ile	Phe	Lys	Leu	Glu	Lys	Phe	His	Trp	Lys	Leu	Ala		
			180					185					190				
Leu	Ser	Val	Ile	Ile	Met	Phe	Val	Gly	Val	Ala	Leu	Met	Val	Phe	Lys		
		195					200					205					
Pro	Ser	Asp	Ser	Thr	Ser	Thr	Lys	Asn	Asp	Gln	Ala	Leu	Val	Ile	Phe		
	210					215					220						
Gly	Ser	Phe	Leu	Val	Leu	Ala	Ser	Ser	Cys	Leu	Ser	Gly	Leu	Arg	Trp		
225					230					235					240		
Val	Tyr	Thr	Gln	Leu	Met	Leu	Arg	Asn	Asn	Pro	Ile	Gln	Thr	Asn	Thr		
			245						250						255		
Ala	Ala	Ala	Val	Glu	Glu	Ser	Asp	Gly	Ala	Leu	Phe	Thr	Glu	Asn	Glu		
			260					265					270				
Asp	Asn	Val	Asp	Asn	Glu	Pro	Val	Asn	Leu	Ala	Asn	Asn	Lys	Met			
		275					280				285						
Leu	Glu	Asn	Phe	Gly	Glu	Ser	Lys	Pro	His	Pro	Ile	His	Thr	Ile	His		
	290					295					300						
Gln	Leu	Ala	Pro	Ile	Met	Gly	Ile	Thr	Leu	Leu	Leu	Thr	Ser	Leu	Leu		
305					310					315					320		
Val	Glu	Lys	Pro	Phe	Pro	Gly	Ile	Phe	Ser	Ser	Ser	Ile	Phe	Arg	Leu		
				325					330					335			
Asp	Thr	Ser	Asn	Gly	Gly	Val	Gly	Thr	Glu	Thr	Thr	Val	Leu	Ser	Ile		
			340					345					350				
Val	Arg	Gly	Ile	Val	Leu	Leu	Ile	Leu	Pro	Gly	Phe	Ala	Val	Phe	Leu		
		355					360					365					
Leu	Thr	Ile	Cys	Glu	Phe	Ser	Ile	Leu	Glu	Gln	Thr	Pro	Val	Leu	Thr		
	370					375					380						
Val	Ser	Ile	Val	Gly	Ile	Val	Lys	Glu	Leu	Leu	Thr	Val	Ile	Phe	Gly		
385					390					395					400		
Ile	Ile	Ile	Leu	Ser	Glu	Arg	Leu	Ser	Gly	Phe	Tyr	Asn	Trp	Leu	Gly		
				405					410					415			
Met	Leu	Ile	Ile	Met	Ala	Asp	Val	Cys	Tyr	Tyr	Asn	Tyr	Phe	Arg	Tyr		
			420					425					430				
Lys	Gln	Asp	Leu	Leu	Gln	Lys	Tyr	His	Ser	Val	Ser	Thr	Gln	Asp	Asn		
		435					440					445					
Arg	Asn	Glu	Leu	Lys	Gly	Phe	Gln	Asp									
	450					455											